

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 4, 2001, 11:35:51 ; Search time 20.95 Seconds  
(without alignments)  
3497,848 Million cell updates/sec

Title: US-09-694-777-3

Perfect score: 5001

Sequence: 1 MTMAGRGRLVAPONTFLEN.....LFEISRPQSESESDIFGAS 962

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4893	97.8	962	I53197	potassium channel
2	4824.5	96.5	989	I48912	potassium channel
3	2563	51.2	1174	A40853	potassium channel
4	2226.5	44.5	934	T42394	potassium channel
5	1452	29.0	1102	T17367	potassium channel
6	1415	28.3	1159	T38465	potassium channel
7	1372.5	27.4	1087	T31300	probable potassium
8	1361	27.2	1017	T31354	probable potassium
9	1322.5	26.4	1284	T13168	probable potassium
10	1100.5	22.0	514	T19579	hypothetical prote
11	469.5	9.4	665	S52072	DmCNGC protein - f
12	439	8.8	695	S74179	cyclic nucleotide-
13	432.5	8.6	664	S11517	cyclic nucleotide-
14	432	8.6	735	I50630	alpha subunit of c
15	429	8.6	706	A55251	cyclic nucleotide-
16	427.5	8.5	732	S35691	cyclic nucleotide-
17	425.5	8.5	663	S11521	cAMP-gated channel
18	419	8.4	887	T03939	potassium channel
19	409.5	8.2	682	I40560	cyclic nucleotide-
20	406	8.1	690	A42161	cAMP-gated cation
21	405.5	8.1	645	I50680	alpha subunit of r
22	404.5	8.1	686	A44842	cAMP-gated ion cha
23	404	8.0	691	JC6509	rod cyclic nucleot
24	402	8.0	807	T12177	potassium channel
25	400	8.0	688	B42161	cAMP-gated cation
26	396.5	7.9	640	S07103	cAMP-gated ion cha
27	395.5	7.9	787	T07052	probable potassium
28	390.5	7.8	575	I59327	potassium channel
29					olfactory cyclic n

30	390.5	7.8	688	2	S55349	potassium channel
31	385	7.7	880	2	F85381	potassium channel-
32	385	7.7	916	2	T05360	probable potassium
33	382.5	7.6	857	2	S62694	potassium channel
34	380.5	7.6	838	2	S23606	potassium channel
35	373.5	7.5	883	2	T07651	potassium channel
36	373	7.5	697	2	H85205	potassium channel
37	373	7.5	697	2	T04931	potassium channel
38	371.5	7.4	662	2	T04461	potassium channel
39	369.5	7.4	772	2	S28292	hypothetical prote
40	368.5	7.4	909	2	S32538	cAMP-gated cation
41	367	7.3	733	2	E85357	hypothetical prote
42	363.5	7.3	800	2	T19627	hypothetical prote
43	361.5	7.2	677	2	S32816	potassium channel
44	360.5	7.2	747	2	T52572	cyclic nucleotide
45	352.5	7.0	738	2	E86294	hypothetical prote

#### ALIGNMENTS

RESULT 1	I53197	1	potassium channel subunit - rat
C:Species:	Rattus norvegicus (Norway rat)		
C:Date:	29-May-1998	#sequence	revision 29-May-1998 #text-change 05-Nov-1999
C:Accession:	I53197		
R:Ludwig, J., Terlau, H., Wunder, F., Bruggemann, A., Pardo, L.A., Marguardt, A., Stuebe, J., 13, 4451-4458, 1994			
A:Title:	Functional expression of a rat homologue of the voltage gated either a go-go		
A:Reference number:	I53197; MUID:95009946		
A:Accession:	I53197		
A:Status:	preliminary; translated from GB/EMBL/DBJ		
A:Molecule type:	mRNA		
A:Residues:	1-962 <RES>		
A:Cross-references:	EMBL:Z34264; NID:g557264; PIDN:CAA84018.1; PID:g557265		
Query Match	97.8%;	Score 4893;	DB 2; Length 962;
Best Local Similarity	97.7%;	Pred. No. 0;	
Matches 940;	Conservative 8;	Mismatches 14;	Indels 0; Gaps 0;
QY	1	MTMAGRGRLVAPONTFLENINIVRSNDTNEVLGNAOIVDMPYISNDGCKLSGYHAEV 60	
DB	1	MTMAGRGRLVAPONTFLENINIVRSNDTNEVLGNAOIVDMPYISNDGCKLSGYHAEV 60	
QY	61	MOKSSTCFMYGELTDKDTIEKVRQTFENYEMNSFELMYKKNRFPWFVKIAPIRNBO 120	
DB	61	MOKSACSFMYGELTDKDTIEKVRQTFENYEMNSFELMYKKNRFPWFVKIAPIRNBO 120	
QY	121	DKVVLFLCTFSITPAFKPIEDDSCKGKGFARLALTSSRGVLOQLAPSVOKGENVHK 180	
DB	121	DKVVLFLCTFSITPAFKPIEDDSCKGKGFARLALTSSRGVLOQLAPSVOKGENVHK 180	
QY	181	HSRLAEVLQSGDILPQYKQEAAPKPPHILHYCVKRTTMDIILTFYTAIVPNYS 240	
DB	181	HSRLAEVLQSGDILPQYKQEAAPKPPHILHYCVKRTTMDIILTFYTAIVPNYS 240	
QY	241	FTTRNNVAMLVVDSIVDVIYFLVDIYLNPHFTFVGAGEVISPDKLRNNYLTQWVIDL 300	
DB	241	FTTRNNVAMLVVDSIVDVIYFLVDIYLNPHFTFVGAGEVISPDKLRNNYLTQWVIDL 300	
QY	301	ISCLPVDVINAENVDGESSLSLKVRLRLRGVARKLDHYTEYGAVALVLAVCVG 360	
DB	301	ISCLPVDVINAENVDGESSLSLKVRLRLRGVARKLDHYTEYGAVALVLAVCVG 360	
QY	361	IAAHMMACTWISIGYEIRDEDTKTIRNNSMLYQLAMDIGTPOFGSSGKWEGPSKN 420	
DB	361	IAAHMMACTWISIGYEIRDEDTKTIRNNSMLYQLAMDIGTPOFGSSGKWEGPSKN 420	
QY	421	SVYISLIVFTMTSLSVGNGTAPSDIEKIFAVAMMGISLLYATIPGNVTTIQOMA 480	
DB	421	SVYISLIVFTMTSLSVGNGTAPSDIEKIFAVAMMGISLLYATIPGNVTTIQOMA 480	

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Db 421 SVYISLFTMTSLTSVGFNAPSTDIKIFAVALMMIGSLITATIGNTTIFQOMTA 480
Qy 481 NTNRYHEMLNSVRDLKLYOVPKGLSERVMDYIVSTWSNRGIDTEKYLQICPKMDADI 540
Db 481 NTNRYHEMLNSVRDLKLYOVPKGLSERVMDYIVSTWSNRGIDTEKYLQICPKMDADI 540
Qy 541 CVHLNRKFKKEHPAFRLASDGLRALAMEFOTVHCAPDLYIHAGESVDSLCEVVGSLLE 600
Db 541 CVHLNRKFKKEHPAFRLASDGLRALAMEFOTVHCAPDLYIHAGESVDSLCEVVGSLLE 600
Qy 601 VIODEVVAIIIGKGVDFGVDFWKEATLAOSCANVRLTYCDLHVTKRDLQVLEFYTA 660
Db 601 VIODEVVAIIIGKGVDFGVDFWKEATLAOSCANVRLTYCDLHVTKRDLQVLEFYTA 660
Qy 661 SHSFERNLILTYNLKRRIVFRKISDVKREEBERMRKNEAPILPPDHPVRLFOFRQO 720
Db 661 SHSFERNLILTYNLKRRIVFRKISDVKREEBERMRKNEAPILPPDHPVRLFOFRQO 720
Qy 721 KEARLAERGGRLDLDLVEKGNVLTERRASANSILVKASVTVRESPTPVSAFASTSG 780
Db 721 KEARLAERGGRLDLDLVEKGNVLTERRASANSILVKASVTVRESPTPVSAFASTSG 780
Qy 781 VPDHAKLAPGSECLGPRKGGDCAKRRKSMARFKDACKSEDMNKVSKAESMETLPERK 840
Db 781 VPDHAKLAPGSECLGPRKGGDCAKRRKSMARFKDACKSEDMNKVSKAESMETLPERK 840
Qy 841 ASGEATLKTSDSCDGIKTSDLRLDNVGEARSPODRSPILAEVKSFFYPPEOTLOATVL 900
Db 841 ASGEATLKTSDSCDGIKTSDLRLDNVGEARSPODRSPILAEVKSFFYPPEOTLOATVL 900
Qy 901 EYRHELEKEDIKALNAKMTNIEKQISEILRLITSRRSSQSPQELFEISRPOSESERDIFG 960
Db 901 EYRHELEKEDIKALNAKMTNIEKQISEILRLITSRRSSQSPQELFEISRPOSESERDIFG 960
Qy 961 AS 962
Db 961 AS 962

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RESULT 2  
148912  
potassium channel subunit - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: 148912  
R:Warme, J.W.; Ganetzky, B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994  
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.  
A:Reference number: A54953; MUID:94211879  
A:Accession: 148912  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-989 <RES>  
A:Cross-references: EMBL:U04294; NID:q487739; PIDN:AAA62474.1; PID:q487740  
C:Genetics:  
A:Gene: m-eag

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Query Match 96.5%; Score 4824.5; DB 2; Length 989;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 933; Conservative 10; Mismatches 19; Indels 27; Gaps 1;

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Qy 1 MTMAGGRGLVAPQMTFLENIVRSNDTFVLGNQIYDMPVIVSNDGFCCKLSGYHRAEV 60  
Db 1 MTMAGGRGLVAPQMTFLENIVRSNDTFVLGNQIYDMPVIVSNDGFCCKLSGYHRAEV 60  
Qy 61 MOKSSTCFMVGELTDKDTIEKVRQTFENYEMNSEFILLYKKNRTPVWFVFIAPIRNDQ 120  
Db 61 MOKSSTCFMVGELTDKDTIEKVRQTFENYEMNSEFILLYKKNRTPVWFVFIAPIRNDQ 120  
Qy 121 DKVVLFLCTFSITAFKOPTEIDSDCKGKCKFRALRALTSSNGVLOOLAPSVOKGENVHK 180  
Db 121 DKVVLFLCTFSITAFKOPTEIDSDCKGKCKFRALRALTSSNGVLOOLAPSVOKGENVHK 180

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Qy 181 HSRLEAVIQLGSDILIPQYKQEAKEPTPHIILHYCVKTTWMIILITFYTALVBNVS 240
Db 181 HSRLEAVIQLGSDILIPQYKQEAKEPTPHIILHYCVKTTWMIILITFYTALVBNVS 240
Qy 241 EKTROMNAMLVYDSIVDYIFLVLDIVLNHTTTFVAGAEVISPDKLRNMYLKTWPIVDL 300
Db 241 EKTROMNAMLVYDSIVDYIFLVLDIVLNHTTTFVAGAEVISPDKLRNMYLKTWPIVDL 300
Qy 301 LSCLPDVVNAFENDE-----GSSLSFSLKVVRLR 333
Db 301 LSCLPDVVNAFENDEVSFAFMQDEKIGFADQIPPLEGRESQGISLSLKVRLR 360
Qy 334 LGRVARKLDHYIEYGAVALVLLVCVGLAAHMACTIWSIGDYEIPEDEDTKITRNSWLY 393
Db 334 LGRVARKLDHYIEYGAVALVLLVCVGLAAHMACTIWSIGDYEIPEDEDTKITRNSWLY 393
Qy 394 QLANDIGTPYQFENGSGGKWEKGSKNVYISSLYFTMTSLTSVGFNAPSTDIKIFA 453
Db 394 QLANDIGTPYQFENGSGGKWEKGSKNVYISSLYFTMTSLTSVGFNAPSTDIKIFA 453
Qy 454 VALMIGSLIYATIFGNMTTIFQOMYANTNRYHEMLNSVRDLKLYOVPKGLSERVMDY 513
Db 454 VALMIGSLIYATIFGNMTTIFQOMYANTNRYHEMLNSVRDLKLYOVPKGLSERVMDY 513
Qy 514 VSTWSNRGIDTEKYLQICPKMDADICVHLNRKVEKEHPAFRLASDGLRALAMEFOTV 573
Db 514 VSTWSNRGIDTEKYLQICPKMDADICVHLNRKVEKEHPAFRLASDGLRALAMEFOTV 573
Qy 574 HCAPGLIYHAGESVSLCEVVGSLLEVIODDVVALIGKGVDFGVFWKEATLAOSCAN 633
Db 574 HCAPGLIYHAGESVSLCEVVGSLLEVIODDVVALIGKGVDFGVFWKEATLAOSCAN 633
Qy 601 HCAPGLIYHAGESVSLCEVVGSLLEVIODDVVALIGKGVDFGVFWKEATLAOSCAN 660
Db 601 HCAPGLIYHAGESVSLCEVVGSLLEVIODDVVALIGKGVDFGVFWKEATLAOSCAN 660
Qy 634 VRALTYCDLHVTKRDLQVLEFYTAFSHFSRNLITLVLRKRYFRKISDVKREEBER 693
Db 634 VRALTYCDLHVTKRDLQVLEFYTAFSHFSRNLITLVLRKRYFRKISDVKREEBER 693
Qy 694 MKRKNAPLILPPDHPVRLFOFRQOKEARLAERGGRLDLDLVEKGNVLTERRASANS 753
Db 694 MKRKNAPLILPPDHPVRLFOFRQOKEARLAERGGRLDLDLVEKGNVLTERRASANS 753
Qy 754 SLVKASVTVRESPTPVSAFASTGVPDHAQLQAPGSECLGPKGGDCAKRSNARF 813
Db 754 SLVKASVTVRESPTPVSAFASTGVPDHAQLQAPGSECLGPKGGDCAKRSNARF 813
Qy 814 KDACGSEDMNKVSKAESMETLPERTKASGEATLKTSDSCDGIKTSDLRLDNVGEARS 873
Db 814 KDACGSEDMNKVSKAESMETLPERTKASGEATLKTSDSCDGIKTSDLRLDNVGEARS 873
Qy 874 ODRSPILAEVKHSFYPIPEOTLOATVLEVRHELEKEDIKALNAKMTNIEKQISEILRLITS 933
Db 874 ODRSPILAEVKHSFYPIPEOTLOATVLEVRHELEKEDIKALNAKMTNIEKQISEILRLITS 933
Qy 934 RNSQSPQELFEISRPOSESERDIFGAS 962
Db 934 RNSQSPQELFEISRPOSESERDIFGAS 962

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RESULT 3  
A40853  
potassium channel protein eag - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 24-Sep-1998  
C:Accession: A40853  
R:Warme, J.; Drysdale, R.; Ganetzky, B.  
Science 252, 1560-1562, 1991  
A:Title: A distinct potassium channel polypeptide encoded by the Drosophila eag locus  
A:Reference number: A40853; MUID:91262635  
A:Accession: A40853  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1174 <MAR>  
A:Cross-references: GB:M61157; NID:g157311; PID:g157312

C:Genetics:  
A:Gene: FlyBase:eag  
A:Cross-references: FlyBase:Fgpn0000535  
C:Keywords: transmembrane protein

Query Match 51.2%; Score 2563; DB 2; Length 1174;  
Best Local Similarity 51.7%; Pred. No. 4e-171;  
Matches 523; Conservative 150; Mismatches 186; Indels 152; Gaps 19;

3 MAGGRGLVAPQNTFLENIVRSN--DTNFVGNQAVDMPIYNSNGPFKISYHNAE 59  
1 MGGRRGLVAPQNTFLENIVRSN--DTNFVGNQAVDMPIYNSNGPFKISYHNAE 60  
60 VMOKSS--TGSFMYGELTDKTEKVRQTFENYEMNSFEILMYKN----- 103  
61 VMOKSRYVGVFMGELTDKTEKVRQTFENYEMNSFEILMYKN----- 120  
104 --RTPVAFVKIAPINEDQKVLFLCTESDITAFKOPIEDSC--GNGKFAIRLTRA 157  
121 QTOETPLMLLQVAPINERDLVYFLFLFRDITALKQPIDSEDTKGVLSKFAKLARS 180  
158 LTRSRGVLOQLAPSVQGENVHKSLAEVLOGLSDLLPQTKQAPKTPPHILHYCFK 217  
181 VTRSR--QFSALPTLKDPKPTKQSNLAHMSLSADIMPOYROEAPKTPPHILHYCAF 236  
218 TTMDMITLLEPTALIVPVNSFKFR--QNNVAVLVDSIVDVIFVDIVLNFHTTFVGP 276  
237 AIMDMVLCIFETALVAPINAVAKNKTSSEVSLVDSIVDVIFVDIVLNFHTTFVGP 296  
277 AGEVISPDKIRNMYLKTWEVIDLSCLPYDVINAFENWEGISLSFSLKVRLLRGR 336  
297 GGEVSDPKVIRNMYLKSFWIFDLSCLPYDVINAFENWEGISLSFSLKVRLLRGR 356  
337 VARKLHIEYGAVALVLYCVGLAAHMAACIWSIGDEIEFEDTKTINNMSLYOLA 396  
357 VVRKLDYLEYGAVALVLYCVGLAAHMAACIWSIGDEIEFEDTKTINNMSLYOLA 411  
397 MDIGTPRQF--NGSGSGKMGKPSKNSVYSSLYFTMTSLTSVGFGLIAPSTDEKIFA 453  
412 NVTQSPSTYVMSNDTGP--ELVNGSPSKSMVYVLTALYFTMTCTSVGFVNAETDEKIFT 470  
454 VALMISGLYATIFGNVTTIFQOMYANTNRYHMLNSVRDFLKLQYPKLSERVMDYI 513  
471 ICMNIIALLXATIFGNVTTIFQOMYANTNRYHMLNSVRDFLKLQYPKLSERVMDYI 530  
514 VSTWMSRGIDTEKVLQICPKDMRADICVHLNRKVRKEHPAFRLASDGLALAMEQTV 573  
531 VSTWAMTKGIDTEKVLQICPKDMRADICVHLNRKVRKEHPAFRLASDGLALAMEQTV 590  
574 HCAPGDLIYAGESVDSLCVSVSSLEVIQDDEVVALGKGVDFWKAATIALQSCAN 633  
591 HSAPEGDLIYAGESVDSLCVSVSSLEVIQDDEVVALGKGVDFWKAATIALQSCAN 650  
634 VRLTYCDLIVIRKDALOKVLEFYTAFSHPSRNLILTYNLRKRIVRKISIDVREEER 693  
651 VRLTYCDLIVIRKDALOKVLEFYTAFSHPSRNLILTYNLRKRIVRKISIDVREEER 710  
694 MKRKNAPLLPPDPVRRILFQFROQKEARLAERGRDL----DLDEVKGNVLETHA 749  
711 ERKNEPQLQNDHLVRKIFSKRRPRPQ---VQAGSKELVYSGSGSDVEKGGGEVVRT 766  
750 SANHSLVKA-----SVYTVRESFAT 769  
767 KV--LPKAKILQASQATTLARODTIDEGEVDSSPPSRDSRVVIEGAAVSATFVGSPRPV 823  
770 PVSGFOASTGVDHAKLQAPGSGCLGPKGGGDCAKRKSMARKKADCGKSEDMNKYSKA 829  
824 ATFTSSAAAGAGVSG-----GPGSGGVVVA-----IYTKA 852  
830 E---SMETLEPRKASGATLKTDCSDGITSKDLRLDNVGEARSPQDRPILAEVYHS 886  
853 DRMLALEREQIMASSRAI--TSDTYDTGL-----KEIPPTLA----- 889

887 EYPIEOTLOATVLEEVYRHELEKEDIKALNAKMTNIEKOLSEILRLTSRRSS 937  
890 -----QRLVAVLDMKVADVRLQLQRMQORIGRIEDLGEIVKRLALPAGSS 935

RESULT 4  
T42394  
potassium channel protein eag homolog - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
R:Accession: T42394  
R:Material: R.  
submitted to the EMBL Data Library, June 1999  
A:Reference number: 222153  
A:Accession: T42394  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-934 <MAT>  
A:Cross-references: EMBL:AF036695; PDB: AAB88348.1  
C:Genetics:  
A:Introns: 27/1; 66/2; 104/1; 147/1; 164/3; 222/2; 263/3; 301/3; 410/1; 468/2; 667/3;  
A:Note: F16B3.1

Query Match 44.5%; Score 2226.5; DB 2; Length 934;  
Best Local Similarity 52.6%; Pred. No. 1.1e-147;  
Matches 447; Conservative 132; Mismatches 194; Indels 77; Gaps 14;

3 MAGGRGLVAPQNTFLENIVRSN--DTNFVGNQAVDMPIYNSNGPFKISYHNAE 60  
1 MGGRRGLVAPQNTFLENIVRSN--DTNFVGNQAVDMPIYNSNGPFKISYHNAE 60  
61 MOKSSTCSFMYGELTDKTEKVRQTFENYEMNSFEILMYKNRTPPVFVKIAPINEDQ 120  
61 MOKPSLAEFMHGEHEVSGISLQMOEALNARTEQAEIGCKRKNKTPIMLVHLAPIKNKR 120  
121 DKVVFELCTESDITAFKOPIEDSCGKGFARLRLATLSNGVLOQLAPSVQGENVYK 180  
121 DAVVLYLQCFKDIPTLKQPLDEN-----NKALCEVYG-----KANAVEE 160  
181 HSRLEAVLOGLSDLLPQTKQAPKTPPHILHYCFEKTWDMVILITLFTYALIVPVNS 240  
161 VTR--VNLGSDMLPQTKQAPKTPPHILHYCFEKTWDMVILITLFTYALIVPVNS 218  
241 EK--TRQN-----NVAMLVDSIVDVIFVDIVLNFHTTFVGPAGEVISPDKIRNMYL 292  
219 FKNSSRENDGGIDSVV--LMDSIYDVIFVDIVLNFHTTFVGPAGEVISPDKIRNMYL 276  
293 KTMFVIDLSCLPYDVINAFENWEGISLSFSLKVRLLRGRVARKDHYIEGAVAL 352  
277 KSMFLIDLSCLPYDVIFYFMKFRDRIEGLFSAKVRLLRGRVARKDHYIEGAVAL 336  
353 VLVVCFGLAAHMAACIWSIGDEIEFEDTKTINNMSLYOLAMDIGTPYQFNGSGSK 412  
337 LLLICAYIVAHMLCQWFIQDSEVRLKMDLALPDGMLKMLSLNDLRQHYINPLSNKTF 396  
413 WEGPSKNSVYSSLYFTMTSLTSVGFGLIAPSTDEKIFAVALIMIGSLATIFGNV 472  
397 LVGGRSRTSAYISSLYYMSGMSVYGFGLIAPSTDEKIFAVALIMIGSLATIFGNV 456  
473 TIFQOMYANTNRYHMLNSVRDFLKLQYPKLSERVMDYIYSTWSMSRGIDTEKVLQIC 532  
473 TIFQOMYANTNRYHMLNSVRDFLKLQYPKLSERVMDYIYSTWSMSRGIDTEKVLQIC 532  
457 TIFQOMYANTNRYHMLNSVRDFLKLQYPKLSERVMDYIYSTWSMSRGIDTEKVLQIC 516  
523 PKDMRADICVHLNRKVRKEHPAFRLASDGLALAMEQTVACAGDILHYAGESVDSLC 592  
517 PKDMRADICVHLNRKVRKEHPAFRLASDGLALAMEQTVACAGDILHYAGESVDSLC 576  
593 FVVSGLSEVIQDDEVVALGKGVDFWKAATIALQSCANVRLATYCDLIVIRKDALQ 651  
577 FVVSGLSEVIQDDEVVALGKGVDFWKAATIALQSCANVRLATYCDLIVIRKDALQ 636

[illegible]

RESULT 5  
T17367  
potassium channel protein elkl - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17367  
R:Shi, W.; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.  
J. Physiol. 511, 675-682, 1998  
A:Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in  
A:Reference number: 218731; MUID:98382545  
A:Accession: T17367  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1102 <SH1>  
C:Cross-references: EMBL:AF061957; NID:g36596689; PID:g3659690; PIDN:AAC61520.1  
C:Genetics:  
A:Gene: elkl  
C:Function:  
A:Description: may play a role in the sympathetic nervous system  
!Keywords: potassium channel

[illegible][illegible]

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RESULT      6
138465      Probable potassium channel subunit - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
C:Accession: 138465
R:Warme, J.W.; Ganetzky, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals
A:Reference number: A54953; MUID:94211879
A:Accession: 138465
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1159 <RES>
A:Cross-references: EMBL:U04270; NID:9487737; PIDN:AAA62473.1; PID:g487738
C:Superfamily: CAMP receptor protein cyclic nucleotide-binding domain homology
F:7.42-858/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CA
Query Match      28.3% Score 1415; DB 2; Length 1159;
Best Local Similarity 30.1%; Pred. No. 1e-90;
Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps 28;

Oy      7 RRGALVAPONTFLENTIVRR-SNDTFNVLGNOIADWPIVYSNDGFCLSGTHRAEVMQKS 64
      ||| ||||| ||| : : : ||| : : ||| ||| ||| ||| :
DB      4 RRGHAAPONTFLDITIRKFEQOSKRFTIANNRVEMCAVIYICNDGFCCLCGSRAEVMDRP 63
      ||| : : : : : : : ||| : : : : : : : ||| : : : : :

Oy      65 STGSCFMYGELTDKDTIEKVRQTFENYEMNSFEILLYKKKRRTPVWFVYKIADIRNEDKVV 124
      ||| : : : : : : : ||| : : : : : : : ||| : : : : :
DB      64 CTCDFLHGPRTQRRAAAOIAQLLGAEEKVEIAFYRDGSCFCLVDVYVVKKNEDGAVI 123
      ||| : : : : : : : ||| : : : : : : : ||| : : : : :

Oy      125 LFLCTFS----- 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      124 MFLNEFVYMEKDWGSPAHDTNHRGPTSWLAPGRATFKLIPALLALTARESSVRSRG 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```





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OY 737 LDVEKGNVLTETHASANSLSVTVRESPTPVSFQASTSGVPDHAQLQAPGSECLG 796
Db 737 -DGEQG-----HTISPPAPA-----DESPPLSPCTSSS--SAAKLSPRTAPR 779
OY 797 PKGGGDCAKRKSMAFRKACGKSEDMNVKSKAESMETLPEPT-----KA 841
Db 760 PLUGRGGRPSRAG-----VLKPEAGPSAHPRLDGLQLPMPWNPDL 823
OY 842 SGEATLKKTDSGSGITKSDRLDNVNG---EARSPODRSPILAEVKSFPYPIEQTLQA 897
Db 824 SPRVVDGIEDGGSDQHKRSFVVGOSGPCSSSPSGTSSGLT-----VPLVPSRA 875
OY 898 TVLEVRHLEKEDIKALNAKMTNIEKOLSEILR---ILTSRSSOSSPO 941
Db 876 RMTDPLDKLRQAVTELSEQVLOMREGIQLROAVQOLILVPGEGGCPR 923

```

```

RESULT 8
T31354
probable potassium channel elk chain 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31354
R:Engelard, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.
submitted to the EMBL Data Library, July 1998
A:Description: Identification of three rat potassium channel genes homologous to D. mela
A:Reference number: 220983
A:Accession: T31354
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1017 <ENG>
A:Cross-references: EMBL:AJ007628; NID:e1329997; PID:e1329998; PIDN:CAA07587.1
A:Experimental source: cortex
C:Genetics:
A:Gene: elk1
C:Keywords: potassium channel

```

```

Query Match 27.2%; Score 1361; DB 2; Length 1017;
Best Local Similarity 33.2%; Pred. No. 5.2e-87;
Matches 330; Conservative 187; Mismatches 323; Indels 154; Gaps 25;

OY 8 RGLVAPQNTFLENIVRSNDT--NFVLGNAQ-IVDMPVIYSNDGFCGLSGYHRAEVWOKS 64
Db 5 KGLLAPQNTFLDTIARFPGTHSNFLLANAGRGPRPIYVCSDFELNGYGRTEVMOKT 64
OY 65 STCSFWYGLTDKDTIEKROTPENTEMNSFELIMYKKNRPVWFVKIAPINEDQKYV 124
Db 65 CSCRLYGETSEPALQRLQKALEGHQEHRAEFCYFRKQGSAPWCLLDMPKINELGEVY 124
OY 125 LFLCTFSDDITAFKOP-----IEDDSCKGWKFARLTRALTSSRGVLOQLA--- 169
Db 125 LFLFSFKDLSQSGGPGCLSGHGDNNHNSLGRGASRLRSTRONRTVLAHRLTGHF 184
OY 170 -----PSVQGENVNRKHSRLAEVLQGLSDILPOLYKQEARPTPHIILHYCVFKTTWMI 224
Db 165 GRDQGSVANKSNVFE-----PKRPSVEPKYVASVGSGLLHLSTIRPAVNDGLI 234
OY 225 LILFTYTAIVPNVNSF-----KTRONNVAMLVVDSTIVDIYFLVDIYLNFTHTVGAPEY 280
Db 235 LLAFTVAVTVVYVNCFAADDPTPISTRHVLSDIAVEMFLIDILNRTVTVYVSSQGV 294
OY 281 ISDPKLRNNYIKTWFTVIDLSCLPYDVINAFENVDEGISLSSFSKVVRLRLGLGVARK 340
Db 295 VSAPISIGLHATWFEVLLALPFDLLIVF-NIT--VTSLVHLKTYKRLLELRLQK 351
OY 341 LDHYLEYGAVALVLCVGLAAHMAACIYSGIDEYFDEDTKTRNNSWMLQALMDIG 400
Db 352 LRRYSGCSAVLTLMSVALLAHMAACWYVIGREM-EANDPLMDIGMHLECKRLE 410
OY 401 TTYQFNGSGKMGGPSNYSYISLVTWMSLTVSGFNALPSTDIKIFAVAIMIG 460
Db 401 TTYQFNGSGKMGGPSNYSYISLVTWMSLTVSGFNALPSTDIKIFAVAIMIG 460

```

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Db 411 EPT-VNGSA-----GSPRSRATIALYFTLLSITSFGPNVCANPDAEIFISCTMLIG 464
OY 461 SLTYATIFGNVNTTIFQOMYANTNRHEMLNSVDPFLKLYOVRGLSERVDYIVSWMS 520
Db 465 ALMHAVVFGVNTALIQRMYSRSLYSRMKDLKDFIVHRLPRLQKRMLEYQTWAVN 524
OY 521 RQIDTEKVLQICPKMRADICVHLNRKVEKEHPAFRLASGCLRALAMEQYVHCAPDL 580
Db 525 SCIDANELLRDPFDELRLADIAHMLNREIL-QLPLFGAASRGCLRALSLHKTSCAPGEF 583
OY 581 IYHAGSVSLCVFVSGSLEVIDDEVAATLIGKDVNG-DV--FMKEATLQAGC-----A 632
Db 584 LLRRGALQAHYVCGSLEVLKDNVTALVIGADLIGADIPELGDEPGAGACVLTSA 643
OY 633 NVBALTYCDLHVIKRDALQVLEFYTAFSHSFERNL--ILTYNLRK----- 676
Db 644 DVKALTYCGLOQLSSRGIAVLRLYPEYVAFRAGLPRLDTFNLROSENNGLGRFSRSP 703
OY 677 RI-----VFRKISDVKKREERMRKKNAPLILPPDHPVRLRFORROOKE 722
Db 704 RLQARSDDLFGSSSDKTLPLSITFEGMEPDAGSKPRRPLLLNLSPAR----- 752
OY 723 ARLAARRGDLDLVEKGNVLTETHASANSLSVTVRESPTPVSFQASTSGVP 782
Db 753 -----PRG-----SLVSLGEEILPPPSALVSSPSLSPSPALAGCSSPSLHGP 798
OY 783 DHAQLQAPGSECLGPKGGGDCAKRKSMAFRKACGKSEDMNVKSKAES--METLPERTK 840
Db 799 RGSAAKPKQLLPLPLGTFRP-PDLSPW-----IVDIEDSSMTAEKAPTRFSAKRPPT 852
OY 841 ASGEATLKKTDSGSGITKSDRLDNVNGEARSPODRSPILAEVKSFPYPIEQTLQATVL 900
Db 853 TRSQAPLS-----GPRLSRLATEAAEEVY----- 877
OY 901 EVRHELEKEDIKALNAKMTNIEKOLSEILRLITSR 934
Db 878 EKVCRNLQETISRLNQEVSQSLRELRQVGLQAR 911

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```

RESULT 9
T31368
probable potassium channel elk chain - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T31368
R:Warme, J.W.; Ganetzky, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals
A:Reference number: A54953; MUID:94211879
A:Accession: T31368
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1284 <MAR>
A:Cross-references: EMBL:U04246; NID:9487735; PID:9487736; PIDN:AAA62472.1
C:Genetics:
A:Gene: elk
A:Cross-references: EMBL:U04246; NID:9487735; PID:9487736; PIDN:AAA62472.1
A:Map position: 2R

```

```

Query Match 26.4%; Score 1322.5; DB 2; Length 1284;
Best Local Similarity 31.8%; Pred. No. 3.7e-94;
Matches 337; Conservative 183; Mismatches 318; Indels 223; Gaps 33;

OY 7 RGLVAPQNTFLENIVRSNDT--NFVLGNAQIVDMPVIYSNDGFCGLSGYHRAEVWOKS 64
Db 4 RGLLAPQNTFLDTIARFPGTHSNFVLGNAQANGNPIYVCSDFVLTGYSRAQIMQK 63
OY 65 STCSFWYGLTDKDTIEKROTPENTEMNSFELIMYKKNRPVWFVKIAPINEDQKYV 124
Db 64 CSCHEFLGPTKEKHQOIKESLSNMEKLEIVFYFKKEGAPFCLDPIPIKNEKRDV 123
OY 125 LFLCTFSDDITAFKOPIE--DDSCKGWGFARLTRLALS----- 160

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```

      111 : 111 : : : 111 111
Db 124 LFLASHRDITHTKM-LENNVNECD--SVFA-LTALLGARFRAGSNAGMLGLGPGIG 179
Oy 161 -----SRGVLOQLAPSVQKGENVHKHSLAEVLQIG 191
Db 180 GPASDDETEGEGNNLDVPAGCMMGRSRRAVLYOLS-----GHYKEKGGVTKKLK 234
Oy 192 SDIL-----POYKQAPKTPPHILHYCVFKTTMDWIIILFFYTAIILVYNSF--K 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 NNFHNSHAPRPPEKTKQSRIKKSRLILPHYGVFKGIMDVILVATFVVALMPYNAFKA 294
Oy 243 TRQNNAMLVDSIVDVILVDIVLNFHTVGPAGEVISDPKILRMNYLKTWVIDLLS 302
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 DRQTKVS---DVIVAEALFVIDILINFRTTFSRKGEVNSKQAIINYLKGMFALDELA 350
Oy 303 CLRPDVINAFENVDGSISSLKVVVLLRGRVARKLDHYIEGAVALVLLVCFGLA 362
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 ALRPDHLASDLYD-GEBSHILVKKLRLRLARLQKIDRYSQHTAMILTLFMSFTLA 409
Oy 363 AHMNACTIY--SIGDYEIFDEDTKTIRNSMWLYOLAMDIGTPYQFNGSGSGKMGSPSKN 420
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 AHMLACTIYVAIVAKVEYEPES-----NIGWLQLLA-----ERKN 444
Oy 421 S-----YISSLFTMTSLTSVGFGNAPSTDIEKIFAVAIMIGSLLYATIFGNV 471
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 445 ASVALITTAETSTALYFTSTLSVGFGNVSAHTAEKFTIIMLIGALMHAVVFGNV 504
Oy 472 TTIRQOYANNRNRYHEMANSRDLFLKYQPKGLSERMDIVSTWMSRGTDETKVLOI 531
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 505 TAILQRMRSRSLYESKMRDLKDVALLNMPKEKQRIEDYFQTSWSLSHGDIETRE 564
Oy 532 CPKMDRADICVHLNRKYFEHAPFLASDGLRALAMEFQVHCAPGLDIYHAGESVSL 591
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 565 FPEELRQDVSHHLREIL-QLPFEASOGCLKLSLHKTNFCAPGEYLHKGKALWYI 623
Oy 592 CEVVSGLSEIVIQDEVAAILGKGVF-----DVEWKEATL 627
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 624 YLLCNGSMVEVTKDMVYVAILGKGLVGSIDINHLVATSNQGMTATTNGADV-----V 677
Oy 628 AQSCANRALTYCDLHYIKRALKOLKYLEFYAFSHSESRNL--ILTYLKRRIYPRKISD 685
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 678 VRSSSDIKALTYCDLCKLHMGLVEVLRLYPEYDOOFANDIOHDLTCMLRE-----G 729
Oy 686 VKREEREMRKKNAPRLIPDPHVRRLFORPROOKEARLAERGRDLDDLDVYKENVL 745
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 YENDSD-----IGSPFLPST-----SEDDENKEAEBSGKG-----EKENGGR 770
Oy 746 TEHASANHSILVKASVTVRESPTPVSFQASTSGVDPHAKLOAGSECLPGKGGGDCA 805
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 771 PSGASPLHNISNPLHATR-SPLIGM-----GSPRNQLHQRGRSLITLR-----E 815
Oy 806 KRKSWARFKDAGCKSEDMNKVSKAESMETLPERKASGEATLKTDCSDGITYNSDLRLD 865
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 816 TNKRHRTLNAAC--SLDRGSFEEPEPLE--EEQSGSGKRPSLERLDQVSTL----- 863
Oy 866 NVGARSROPDSPLIAEKHSFYRIPQTLQATVLEVNHELK-----EDIKALNAKMT 918
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 864 -----HODVAQLSAEVRNAISALQEMFTTSNMTSHSSKLPFPAKSIPIINISGAGTRS 916
Oy 919 NIEKO---LSEIL---RLTTSRRSSQPOELF--EISRPQS 951
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 917 GVAVEHGLMGVLAALAEALAMQRSSSHPEVWAGRDVQLPTS 957

```

RESULT 10  
 T19579  
 hypothetical protein C30D11.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19579  
 R:Mortimore, B.  
 submitted to the EMBL Data Library, August 1994  
 A:Reference number: Z19145

```

A:Accession: T19579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-514 <M1>
A:Cross-references: EMBL:Z35596; PIDN:CAA84644.1; GSPDB:GN00021; CESP:C30D11.1
A:Experimental source: clone C30D11
C:Genetics:
A:Gene: CESP:C30D11.1
A:Map position: 3
A:Introns: 49/3; 77/2; 151/3; 192/3; 244/2; 264/1; 366/3; 435/2; 479/1

Query Match      22.0%; Score 1100.5; DB 2; Length 514;
Best Local Similarity 43.4%; Pred. No. 3.3e-69;
Matches 222; Conservative 104; Mismatches 143; Indels 43; Gaps 12;

Oy 159 TSSRCV-----LQOLAPSVQKGENVHKHSLAEVLQIGSDILPOLYKQAPKTPPHIL 211
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 TSSGAGNAVASQAKOLMVLQSGS-----YKVLISGADVLPEYKLPQPRHHCCTIV 74
Oy 212 HCVFETKTDWIIILFTFTALIVPNVSEKTRQ--NNVA-----WLVDSIVDVIFL 262
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 HSPFRAVMDWIIILLVITTAFTPYVAALFLKELODTAKSRFTEPLEIVDLIVDMFT 134
Oy 263 VDIVLNFHTFVG---PAGEVISDPKILRMNYLKTWVIDLLSCLPYDVINAFENVDGI 319
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 VDIILNFTTYVNDENACQVVSDDPKIATHYKFGFIIDMAAAYFDDLIVSTNDE--T 193
Oy 320 SLESSLKVVRLRLGRVARKLDHYIEGAVALVLLVCFGLAAHMACTIWSIGDYEIF 379
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 TLLIGLTKARLRLRVARVARKLDHYIEGAVALLLMAFFALIAHMLACTIWAIGSAEL- 252
Oy 380 DEDTIRNNSMWLYOLAMDIGTPY-QFNGSGSKMGSGSKSVYISLFTFTSLTSVG 438
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 -----SHKEYTWLHOLSKOLAQPYSTNGTIP--TGSPFLSRVYTSLYFTSLTSTIG 304
Oy 439 FGNIPSTDIEKIFAVAIMIGSLYATIFGNVTTIFQOYANTNRNRYHEMANSRDLFLK 498
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 FGNVSNATDSEKIFITIMHILGSLMAYSVFGNVAILOGLSTARYHEMSRLREFIR 364
Oy 499 YQVPGKLSERVMDIVSTWMSRGTDETKVLOICPKMDRADICVHLNRKYFEHAPFLA 558
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 HQIPNPLRQRLREYFQHAWSYNGIDMNLVLRKGFPCLDADICLHNRMLISGCAAFAGS 424
Oy 559 SGGCLRALMEQTYHCAAGDLIYHAGESVDSLCFVVSGLSEIVQDE--VVALIGKGVF 617
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 TPGCLRALSMRPRTHSPGDLVHRGDLITGLYFARGSVEILANDNTVMGILGKDIF 484
Oy 618 GD--VFWKEATLAOSCANRALTYCDLHYIKR 647
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 GENPLLYDE--VGKSSCNVRAULTYCDLHKILR 514

```

RESULT 11  
 S52072  
 DMCNCG protein - fruit fly (*Drosophila* sp.)  
 C:Species: *Drosophila* sp.  
 C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Jul-1999  
 C:Accession: S52072  
 R:Baumann, A.; Frings, S.; Godde, M.; Selfert, R.; Kaupp, U.B.  
 EMBO J. 13, 5040-5050, 1994  
 A:Title: Primary structure and functional expression of a *Drosophila* cyclic nucleotid  
 A:Reference number: S52072; MUID:95045396  
 A:Accession: S52072  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-665 <BAU>  
 C:Genetics:  
 A:Gene: FlyBase:Cng  
 A:Cross-references: FlyBase:FBgn0014462  
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleoti  
 F:429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA

Query Match 9.4%; Score 469.5; DB 2; Length 665;  
Best Local Similarity 25.0%; Pred. No. 7.9e-25;  
Matches 165; Conservative 110; Mismatches 241; Indels 143; Gaps 25;

```
OY YHRAVAMKSSCSMCELTGKDTIEKVRQFENVENMSFILLWKKRR--TPWEPFK 112
DB 3 HFKKAMVQSDISATIGQDTAEPSKSKPSALRRITQALRQRLRRPRPPQFLEK 62
OY 113 IAPINBODKVVLFCTFSDITAFKQPIEDDSCGKGKFARLTRALTSRGVLOQLAPSV 172
DB 63 FSNTTN-TDK-----I 72
OY 173 OKGENVHKSHSLAEVLQGLSOLPOLYKODAPKTPPHILHVCFTWDMILITFYTA 232
DB 73 RKGCPAMEDAALSSER-GSSVLCNRLSVDPQLQSH-----YMLAIV-----S 115
OY 233 ILVPVNSFKTRQ-----NNVA--WLVVDSIVDVIPLVDIVLPHFTFVGPAGEVID 283
DB 116 LAVLNLILFVVGRAVFWMEINKSAPAFWYTLIDYLCDFIYLDLVHMHGFL-DOGLVARD 174
OY 284 PKLIRMYLKT--WFIIDLCLPYDVINAFENVDEGISLSSLKVV---RLRLGVRV 337
DB 175 AFRLRNHFHTKGMV-LOVLSMLPTDLATYMW-PPETGSSILYPCPVYRLRLRLRL 232
OY 338 ARKLD-----HYEYGAIVLVLCVFGIAAHMACIWSIGDYEL-FDEDTKTR 387
DB 233 WEMFDETFATGYPNAPFRICKVLAIVLVL-----HMNACMFAL-SYEIGFSSD----- 281
OY 388 NNSMLYOLAMDIGTPYOPNGSGSGKMGSPKNSV---YISSLYFTMSLTSVGCNINAP 444
DB 282 --SWYTNL-----NCTRNNTLOROVITYSPYSTLLTYLTIG-ETPPR 319
OY 445 STDIKIFAVAILMIGSLTYATIFGNVTTIFQOMYANTNRHYEMLSNVDFPLKIVOPRG 504
DB 320 ENDVYILFVAVDFLAGVILFATIVGNIGSMISNMVAREFQNRKDGQVQYMAFRVNGH 379
OY 505 LSERYMDYIVSTWMSKRGIDTEKVLQICPKRADICVHLNKKVKEHNPFRILASDGLR 564
DB 380 LEARVIRFAYTWOSGALDEERVLALPDKLAEIAGVHMDTLKQVAFIDHTEGILLE 439
OY 565 ALAMFQVHCHAPGDLIYHAGESVSLCFYVSGSELYIODD--EVVALIGKDVGDVW 622
DB 440 ALVTLKLQVSPGDIYCKRGDVGKEMVYIKRGKLSVWGDDITVLTATGAGSVFGEVS 499
OY 623 KE---ATLAOSCANVRALTYCDLHVY-KRDALOKVLEFYAFSHSFNLLITYLWR 676
DB 500 LEIAGNRTGNRTANVRSLGYSDLCIAKRDLMEIYLPKARSTLTGRCOL---LRK 555

RESULT 12
S74179
Cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 393, 211-215, 1996
A:Title: Molecular cloning, functional expression and chromosomal localization of a human
A:Reference number: S74179; MUID:96409310
A:Accession: S74179
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YMW>
A:Experimental source: retina
C:Genetics:
A:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAR>
```

Query Match 8.8%; Score 439; DB 2; Length 695;

Best Local Similarity 24.7%; Pred. No. 1.2e-22;  
Matches 141; Conservative 110; Mismatches 225; Indels 96; Gaps 17;

```
OY 199 KOEAPKTPPHILHVCFTWDMILITFYAIVLVVNSFKTRQNN--VAVLVVDSI 256
DB 155 KDAIVDVSSNLY-----RWLTALALPFIYMYILLICACADELQSEVLMVLDVS 209
OY 257 VDVILFVILVPHFTFVGPAGEVIDPKLRMY-LKTFWFIIDLCLPYDVINAFENV 315
DB 210 ADVLVLDVILVARTGFL-EOGLMVSQDTRLMQHYKTQFKLDVLSLVPTDL--AVLK 266
OY 316 DEGISLSSLKAVVRLRLGRVARKID-----HYEYGAIVLVLCVFGIAAHM 366
DB 267 ---GNYPEVRNRLKESRLEFEFDRTRNYPMPFRIGLVYILLI-----HMN 317
OY 367 ACTIWSIGYEIPEDEPKTIRNNSMLYOLAMDIGTPYOPNGSGSGKMGSPKNSVYISS 426
DB 318 ACTYFAISKFIQGTG-----SWYTP--NISTEP--HGRLSRK-----YIYS 335
OY 427 LYFTMTSLTSVSGFNAPSTDIKIFAVAILMIGSLTYATIFGNVTTIFQOMYANTNRH 486
DB 356 LVMSTLTLTIG-ETPPVYVDEEYLFVYVDFLVGLVIFATIVGNIGSMISNMASRAEFQ 414
OY 487 EMINSYRDLKLYQVKGISERYMDYIVSTWMSKRGIDTEKVLQICPKRADICVHLN 546
DB 415 AKDISIKQYQFQKRYKTDLETBYIRFMDYLMANKKYDEKEVLSLPDKLAEIAINVL 474
OY 547 KYVEKHPARILASDGLRALAMEFQVHCHAPGDLIYHAGESVSLCFYVSGSELYIODE 606
DB 475 DYLKRIIFQDCAGALVELVLRPPVSPGDIYCKGIGKEMVYINBKLAIVAADG 534
OY 607 VV--AIIKGVDFGVFWKEATLAOS---CANVRALTYCDLHVYIKRDALOKVLEFYTA 660
DB 535 VQGFVVLSDGSYVGEISILNIGSKSGNRTANIRSGYDLCISDDLMELATEPQ 594
OY 661 S---HSFSNLLITYNLKRRIVFKKISDYKREBERMKKNAPLILPDPHFYRLFOR 716
DB 595 AKKALEEKGRQILMKNDLDEBLRAGADPKLEEK----- 630
OY 717 FROQKEARLAEGRGRLDLDVEKGVNLEH 748
DB 631 -----VBOGSSLDLTQTRFARLAEY 652
```

```
RESULT 13
S11517
Cyclic nucleotide-activated channel protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C:Accession: S11517
R:Dhallan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.
Nature 347, 184-187, 1990
A:Title: Primary structure and functional expression of a cyclic nucleotide-activated
A:Reference number: S11517; MUID:90370115
A:Accession: S11517
A:Molecule type: mRNA
A:Residues: 1-664 <DHA>
A:Cross-references: GB:X5519; NID:956791; PID:CA39135.1; PID:956792
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleoti
C:Keywords: transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA
```

Query Match 8.6%; Score 432.5; DB 2; Length 664;  
Best Local Similarity 25.1%; Pred. No. 3.1e-22;  
Matches 144; Conservative 98; Mismatches 227; Indels 105; Gaps 19;

```
OY 220 WDFIILIFPYTALVVPVNSFKTRQNN--VAVLVVSIYDVILVIVLPHFTFVGPA 277
DB 145 WLFVIAFVILYNNCLVAVACFSDLQNRVYVWLVDYSDYIADLIIRLTGFL-EG 203
OY 278 GEVISDPKLRMYLKT-WFVIDLCLPYDVINAFENVDEGISLSSLKVVRLRLGR 336
```

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Db 204 GLLVQDKPLKLDNIHTLQFKLDVASIIPDIL-----YFVAGHS--PEVRPNRLHFAH 257
QY 337 VARRLD-----HYIEGAVALVLLVCVGLAHMAMCIWYSIGDYEFDEDTKIR 387
Db 258 MFEFDDTERTYSPNIFRISNLVLYLII-----HMNCIYVVISKISGFDY----- 308
QY 388 NMSMLYQLANDIGTPYQFNGSGSGKMGCPKNSVYISLFTYMTSLTSVGFNGIAPSTD 447
Db 309 ---WVYINIDPEXGLAR-----EYIYCLVWSTLLTLTTIG-ETRPVVKD 349
QY 448 IEFIFAVAIMIGSLLYATIFGNVTTIFQOMYANTNRYHEMLNSVROFLKLYQVPGKISE 507
Db 350 EEFLEVFDFDLIGVLIATFATVGNVSMISMMNATRAEFOAKIDAVKHMOPRKVSKDMEA 409
QY 508 RMDYIYSTMSKCIDTEKVLQICPKDMRADICVHLNRKVFKEHPAPRLASDGLRALA 567
Db 410 KVIKMFYLTNKTVDEREVLKMLPAKLRAELINVHLSTLKVRIFOCEAGLLELV 469
QY 568 MERQVHCAFGLLYHAGESVDSLCFVVSGLSEYIODEVY--AIIKGVDFGVF--W 622
Db 470 LKLRPQVSPGDYICRKGDIKEMKIIEKGLAVADDGYQVALLSAGSCFGEISLINI 529
QY 623 KEATFLA-QSCANVRLTYCDLHVTKRDLQKLEFYTAFSHSESRNLILTYNLRKRIYER 681
Db 530 KGSKMGRRTANIRSLGSDLFCLSKDDLMEAVTEY----- 565
QY 682 KIDVYKREER-----MKR-----KNEAPLILPDHVRRLRQFROOKEARLAERGR 732
Db 566 --DPAAKVLDERGRELIMKSGLDENEVAAAMEVD-----VOEKLEOLET----- 608
QY 733 DLDDIDVEKGNVLEHASANHSILYKASVYVRES 766
Db 609 NMDLTYRFARLAELYGAQOKLQR--ITVLEF 640

RESULT 14
150630
alpha subunit of cone photoreceptor CNG-channel - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: 150630
R:Boungk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.E.
Neuron 10, 865-877, 1993
A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A:Reference number: 150630; MUID:93264082
A:Accession: 150630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-735 <BON>
A:Cross-references: EMBL:X89598; NID:g908850; PIDN:CAA61757.1; PID:g908851
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

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Query Match 8.6%; Score 432; DB 2; Length 735;  
 Best Local Similarity 25.9%; Pred. No. 3.9e-22;  
 Matches 143; Conservative 108; Mismatches 226; Indels 76; Gaps 19;

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QY 197 QYQKQAPKTPPHIILHYCVFKTWDMIIILTFYATLVPVNSFKTRQ--NNVAVLVD 254
Db 195 EQKREYVVIDPSSNMY-----NMULTIARVFNWCMILCRACFDELQIDHILMLFLD 249
QY 255 SIYDVIFLVDIVNFHTFVGPAGEVISDPKLIRMYLKT-MFVIDLSCLLPDVINAFE 313
Db 250 YCSDIIVFDMFVFRGFL-EGGLVAVKDEKLDHDTQVQFLDLVLSLPTDL--AYL 306
QY 314 NWDEGISLSSLKAVVLLKGRVAKLD-----HYIEGAVALVLLVCVGLAAH 364
Db 307 KL--GLN--YPLERFNRLIARLEFFEDRTERTNPNMFRINLVLYLIIII--H 357
QY 365 WMACIWSIGDYELFDDDTIRNNSMLYQLANDIGTPYQFNGSGSGKMGCPKNSVYI 424
Db 358 WMACIYFAISKVIGFGD-----SMVYP--NVSIPY--GRLSRK-----YI 395

```

```

QY 425 SLVPTMTSLTSVGFNGIAPSTDIEKIFAVAIMIGSLLYATIFGNVTTIFQOMYANTNR 484
Db 396 YSLVSTLTLTTIG-ETRPVVKDEELFVVIDFVGLVFATFATVGNVSMISMMNARSAB 454
QY 485 YHEMLNSVROFLKLYQVPGKISERVMDYIVSTWSRSGIDTEKVLQICPKMRADICVHL 544
Db 455 FOAKVDSIKOYWHFRKVKLDLEARVLIKMFEDYLMTKKTKVDEKEVLKMLPDKLKAETAINV 514
QY 545 NRKVFKEHPAPRLASDGLRALAMEFQVYHCAFGDLIYHAGESVDSLCFVVSGLSEYIOD 604
Db 515 HLDTLKVRITFQDCEAGLITELVLLKLPVSPGDYICKRGDIGREMYTIKRGKLAIVAD 574
QY 605 DEVY--AIIKGVDFGVFKREATLAOS-----CAVNRALTYCDLHVTKRDLQKYLEFYT 658
Db 575 DGIITPVVLSGDSYGEISILNIKSGSKNRTANIRSGISYDLCISDDLMLEALTEP 634
QY 659 AFHSF---SRNLILTYNLRKRIYERKISDVREERERKRNAPLILPDHVRRLRQ 715
Db 635 EAKKALEERGRQILKMDNLIDEAAKAGADPK-DLEEKIDRLFTALDTL----- 682
QY 716 RFRQOKEARLAE 728
Db 683 ---QTRFARLLAE 692

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RESULT 15  
 A55251  
 cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 13-Aug-1999  
 C:Accession: A55251; S43976  
 R:Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994  
 A:Title: Another member of the cyclic nucleotide-gated channel family, expressed in t  
 A:Reference number: A55251; MUID:94224768  
 A:Accession: A55251  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-706 <BIE>  
 A:Cross-references: GB:X76485; NID:g488728; PIDN:CAA54023.1; PID:g488729  
 A:Experimental source: kidney  
 R:Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H. Nature 368, 859-863, 1994  
 A:Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from  
 A:Reference number: S43976; MUID:94211295  
 A:Accession: S43976  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-706 <WEY>  
 A:Cross-references: GB:X89600; NID:g908823; PIDN:CAA61759.1; PID:g908824  
 A:Experimental source: testis  
 C:Genetics:  
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleoti  
 C:Keywords: cAMP binding, ion channel, ion transport, membrane protein  
 F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA

Query Match 8.4%; Score 429; DB 2; Length 706;  
 Best Local Similarity 23.4%; Pred. No. 5.9e-22;  
 Matches 146; Conservative 128; Mismatches 245; Indels 104; Gaps 21;

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QY 173 QKGEVNHKSLAEVLQGSDDLPOYQKQAPKTPPHIILHYCVFKTWDMIIILTFYTA 232
Db 163 EKKEPKKEEK-----KKDSVYMDSSNMY-----HMLTVAIVVFYVW 202
QY 233 ILVYVNSFKTRQNN--VAVLVDSIVDVIFLVDIVLNFHTFVGPAGEVISDPKLIRMN 290
Db 203 CLVCRACFDELQSHMLMLVLDYSADILYGMVLVRAKFTL-EGGLMVMDASRLMKH 261
QY 291 YLKT-MFVIDLSCLLPYVINAFENVDSISLSSLKAVVLLRGRVAKLD----- 342

```

```
Db 262 YTOTLHFKEIDVLSVPTDL--AYFKL--GMN--YPELRFNRLKLARLEFFEDRTETRN 315
QY 343 --HYIEYGAVALVLVCVFGLAHMACIMYSIGDYEIEFDEDTKTRINNWSMLYOLAMDIG 400
Db 316 YPNMFRIGNLVLYIILII-----HWNACIYFAISKFIGFTD-----SWYYP---NVS 360
QY 401 TPYOENGSGSGKMEGSPKNSVYISLFTMTSLTSVGFNGIAPSTDIKIPAVAIMIG 460
Db 361 NPEY--GRLSRK-----YISLWSTLTLTIG-ETPPVYKDEEYLFVVIDFLVG 407
QY 461 SLVATTINGVTTIFQOMVANTNRHEMINSVRDLKLYOYKGLSERVMDYIVSTWSMS 520
Db 408 VLIPTATLVGNVSMISNMNASPAEQAKIDSIKQYMOFRKVTKDLETRVIRWFDYLMANK 467
QY 521 RGIPTKVIQICPKDMRADICVHLNRKVFKEHPAFRLASDCGLRALAMEFQVHCAPGDL 580
Db 468 KTYDEKEVYKSLPKLKAELAINVHLDLTKRKRIQDCEAGLLVELYVCLKRAVFSPGDY 527
QY 581 IYHAGESVDSLQFVVSGSLEYIODEVY--AIIKGQVFGDVFWKEATLAQS---CANV 634
Db 528 ICKGDIQREMYIIEKGKLAVAEDGITQFVVLGDGSYFGEISILINIKSGSKGNRRTANI 587
QY 635 RALFYCDLHVYIKRDLQVLEFYTAFSHF---SRNLITVYNLKRRIVFRKISDYKREE 691
Db 588 RSIQISDLFLCLSKDDLMELTEYPAKKALEEKGROIIMKDNLIDDELAKAGADPRDIE 647
QY 692 --ERMKRKEAPLILPPDHPVRLFORPQOKEARLAAERGGRLDDLDVEKGNVITEHA 749
Db 648 KVEHLETSLS-----LQTRFARLLAEYNATQMK-----VKQRL 681
QY 750 SANHSLVAKASVTVRESPTPVS 772
Db 682 SOLESQVKKGLPPDGDAPQTEAS 704
```

Search completed: August 4, 2001, 11:38:05  
Job time: 134 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2001, 11:36:21 ; Search time 34.31 Seconds

(without alignments)  
3709.631 Million cell updates/sec

Title: US-09-694-777-3

Perfect score: 5001

Sequence: 1 MTMAGRGRLVAPONTFLEN.....LFEISRPSPESERDIFGAS 962

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_mammal:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_unclassified:\*  
14: sp\_vertebrate:\*  
15: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5001	100.0	962	4	076035 homo sapien
2	4977.5	97.8	989	4	095259
3	4893	97.8	962	11	063472
4	4842	96.8	960	6	018965
5	4824.5	96.5	989	11	060603
6	4818.5	96.4	987	6	018966
7	3775.5	75.5	988	11	09EP19
8	3767.5	75.3	988	11	09H252
9	2565	51.3	1174	5	09VX26
10	2250.5	45.0	956	5	09VX27
11	2226.5	44.5	934	5	044164
12	1471.5	29.4	950	11	054853
13	1468.5	29.4	994	4	09H252
14	1452	29.0	1102	11	088877
15	1435.5	28.7	1195	11	09ER47
16	1433.5	28.7	1195	11	054852
17	1429	28.6	1163	11	008962
18	1426.5	28.5	1162	11	035221
19	1418	28.4	1158	6	09TS23

20	1413.5	28.3	1162	11	035219	035219 mus musculu
21	1408	28.2	1196	4	09NS40	09NS40 homo sapien
22	1378.5	27.6	1144	6	019119	019119 oryctolagus
23	1372.5	27.4	1087	11	089047	089047 rattus norv
24	1369	27.4	1017	4	09U005	09U005 homo sapien
25	1369	27.4	1083	4	09U006	09U006 homo sapien
26	1369	27.4	1117	4	09U008	09U008 homo sapien
27	1367.5	27.3	1087	11	09UW20	09UW20 mus musculu
28	1365	27.3	1017	11	09R179	09R179 rattus norv
29	1361	27.2	1017	11	089048	089048 rattus norv
30	1322.5	26.4	1284	5	023974	023974 drosophila
31	1322.5	26.4	1311	5	09V899	09V899 drosophila
32	1266.5	25.3	820	11	035989	035989 mus musculu
33	1261.5	25.2	888	4	09H3P0	09H3P0 homo sapien
34	1253.5	25.1	820	11	035220	035220 mus musculu
35	1196.5	23.9	791	5	09NG78	09NG78 caenorhabdi
36	1170.5	23.4	855	5	002497	002497 drosophila
37	1100.5	22.0	514	5	018325	018325 caenorhabdi
38	1095.5	21.9	526	13	09PT84	09PT84 gallus galli
39	729.5	14.6	366	11	09QW68	09QW68 rattus norv
40	687	13.7	141	11	088893	088893 rattus norv
41	520	10.4	837	6	09WZ51	09WZ51 oryctolagus
42	512.5	10.2	910	11	054859	054859 mus musculu
43	512.5	10.2	910	11	088704	088704 mus musculu
44	512	10.2	910	11	09JXB0	09JXB0 rattus norv
45	506	10.1	1203	4	09Y3Q4	09Y3Q4 homo sapien

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	962 AA.
076035				
ID	076035			
AC	076035			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)			
DE	PORASSIUM.CHANNEL.H-EAG.			
GN	EAG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SKLETAL MUSCLE;			
RX	MEDLINE=98408853; PubMed=9738473;			
RA	Occhiodoro T., Bernheim L., Liu J.H., Bijlenga P., Smanrich M.,			
RT	Bader C.R., Fischer-Loughned J.Y.,			
RT	"Cloning of a human ether-a-go-go potassium channel expressed in			
RT	myoblasts at the onset of fusion."			
RL	FEBS Lett. 434:177-182(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Pardo L.A., del Camino D., Sanchez A., Beckh S., Stuhmer W.;			
RT	"Abnormal expression of human eag K+ channels in cancer cell lines			
RT	from diverse origin."			
RL	Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AJ001366; AAC04700.1;			
DR	EMBL: AF078741; CAC08668.1;			
DR	InterPro: IPR000014;			
DR	InterPro: IPR000595;			
DR	InterPro: IPR000636;			
DR	InterPro: IPR000700;			
DR	InterPro: IPR001610;			
DR	InterPro: IPR001622;			
DR	InterPro: IPR020253;			
DR	Pfam: PF00027; CNMP_binding; 1.			
DR	Pfam: PF00785; PAC; 1.			
DR	Pfam: PF00914; CNG_membrane; 1.			
DR	PROSITE: PS50042; CNMP_BINDING_3; 1.			
DR	SMART: SM00100; CNMP; 1.			



KW Ionic channel.  
SQ SEQUENCE 962 AA; 108596 MW; 9CC995A9F156582D CRC64;

Query Match 100.0%; Score 5001; DB 4; Length 962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPYVSNDFCKLSGYHRAEV 60  
DB 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPYVSNDFCKLSGYHRAEV 60  
QY 61 MOKSSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKRNPVWFVKIAPIRNEQ 120  
DB 61 MOKSSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKRNPVWFVKIAPIRNEQ 120  
QY 121 DKVYFLCTFSDITAFKQPIEDDSCGKGKFAFLTRALTSRGVLOOLAPSVQKGENVHK 180  
DB 121 DKVYFLCTFSDITAFKQPIEDDSCGKGKFAFLTRALTSRGVLOOLAPSVQKGENVHK 180  
QY 181 HSRLAEVLQGLSDILPOYKQAPKTPPHIILHYCVFKTTMDIILITFEYFALVLPYVNS 240  
DB 181 HSRLAEVLQGLSDILPOYKQAPKTPPHIILHYCVFKTTMDIILITFEYFALVLPYVNS 240  
QY 241 FKTQNNVAVLVDSIVDVIPLVDIVLNFHTTGVGAGEVISDPKILRMNVLKTFEVIDL 300  
DB 241 FKTQNNVAVLVDSIVDVIPLVDIVLNFHTTGVGAGEVISDPKILRMNVLKTFEVIDL 300  
QY 301 LSCLPYDVINAFFENVDEISLSFSLKAVRLRLGRVARKLDHYIEYGAAYLVLLVCVFG 360  
DB 301 LSCLPYDVINAFFENVDEISLSFSLKAVRLRLGRVARKLDHYIEYGAAYLVLLVCVFG 360  
QY 361 LAAMHMACIWSIGDYEFDEDTKTRNNSMYLOLAMDIGPYONGSGSGKWEKGPSSKN 420  
DB 361 LAAMHMACIWSIGDYEFDEDTKTRNNSMYLOLAMDIGPYONGSGSGKWEKGPSSKN 420  
QY 421 SVYISLSYFTMTSLTSVGFNGIAPSTDIETKIFAVAIMMIGSLVATIFGNTTIFQOMYA 480  
DB 421 SVYISLSYFTMTSLTSVGFNGIAPSTDIETKIFAVAIMMIGSLVATIFGNTTIFQOMYA 480  
QY 481 NTNRYHEMLNVSROFLKIYQVPGKISERVMDYIVSTWMSKRIIDEXVLQICPKMRADI 540  
DB 481 NTNRYHEMLNVSROFLKIYQVPGKISERVMDYIVSTWMSKRIIDEXVLQICPKMRADI 540  
QY 541 CVHLNRKFKFHPAFRLASDGLRALAMEFQVHCAPGDLIYHAGESVDSLCFVVSGL 600  
DB 541 CVHLNRKFKFHPAFRLASDGLRALAMEFQVHCAPGDLIYHAGESVDSLCFVVSGL 600  
QY 601 VIODEVVAIIGKGDVDFGVFWKEATLAQSCANVRALTYCDLHVTKRDALQVLEFYTA 660  
DB 601 VIODEVVAIIGKGDVDFGVFWKEATLAQSCANVRALTYCDLHVTKRDALQVLEFYTA 660  
QY 661 SHSSSRNLIILYNNLRKRYVFRKISVYKREERBMKRNKNEAPILPDPHVRLPQRFROQ 720  
DB 661 SHSSSRNLIILYNNLRKRYVFRKISVYKREERBMKRNKNEAPILPDPHVRLPQRFROQ 720  
QY 721 KEARLAERGRDLDLVEKGNVLTJHASANHSVYKASVYTVRESPPVPSFOAASVSG 780  
DB 721 KEARLAERGRDLDLVEKGNVLTJHASANHSVYKASVYTVRESPPVPSFOAASVSG 780  
QY 781 VPDAKLOAPGSECLGPKGGGDCAKRKSMARFKDACKGSEDMNVKSAKESMETLPERTK 840  
DB 781 VPDAKLOAPGSECLGPKGGGDCAKRKSMARFKDACKGSEDMNVKSAKESMETLPERTK 840  
QY 841 ASGEATLKTTSOCSGKITKSDRLDNVGBANSPODRSPILAEVKSFTPIPQOTQATV 900  
DB 841 ASGEATLKTTSOCSGKITKSDRLDNVGBANSPODRSPILAEVKSFTPIPQOTQATV 900  
QY 901 EVRHEIKEDIALNAKMNIEKQISEILRIITSSRSSOSPQLFEISRSQSESESDIFG 960  
DB 901 EVRHEIKEDIALNAKMNIEKQISEILRIITSSRSSOSPQLFEISRSQSESESDIFG 960  
QY 961 AS 962

DB 961 AS 962

RESULT 2  
ID 095259 PRELIMINARY; PRT; 989 AA.

AC 095259;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE VOLTAGE-GATED POTASSIUM CHANNEL EAGB.  
GN EAG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Pardo L.A., del Camino D., Sanchez A., Beckh S., Stuhmer W.;  
RT "Abnormal expression of human eag K+ channels in cancer cell lines  
from diverse origin.";  
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF078742; AAC68669.1; -;  
DR InterPro: IPR000014; -;  
DR InterPro: IPR000595; -;  
DR InterPro: IPR000636; -;  
DR InterPro: IPR000700; -;  
DR InterPro: IPR001610; -;  
DR InterPro: IPR001622; -;  
DR InterPro: IPR020205; -;  
DR Pfam: PF00027; CNMP\_binding; 1.  
DR Pfam: PF00785; PAC; 1.  
DR Pfam: PF00914; CNG membrane; 1.  
DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
DR SMART: SM00100; CNMP; 1.  
KW Ionic channel.  
SQ SEQUENCE 989 AA; 111422 MW; CAA8CB251300C7E5 CRC64;

Query Match 99.5%; Score 4977.5; DB 4; Length 989;  
Best Local Similarity 97.3%; Pred. No. 0;  
Matches 962; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPYVSNDFCKLSGYHRAEV 60  
DB 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPYVSNDFCKLSGYHRAEV 60  
QY 61 MOKSSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKRNPVWFVKIAPIRNEQ 120  
DB 61 MOKSSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKRNPVWFVKIAPIRNEQ 120  
QY 121 DKVYFLCTFSDITAFKQPIEDDSCGKGKFAFLTRALTSRGVLOOLAPSVQKGENVHK 180  
DB 121 DKVYFLCTFSDITAFKQPIEDDSCGKGKFAFLTRALTSRGVLOOLAPSVQKGENVHK 180  
QY 181 HSRLAEVLQGLSDILPOYKQAPKTPPHIILHYCVFKTTMDIILITFEYFALVLPYVNS 240  
DB 181 HSRLAEVLQGLSDILPOYKQAPKTPPHIILHYCVFKTTMDIILITFEYFALVLPYVNS 240  
QY 241 FKTQNNVAVLVDSIVDVIPLVDIVLNFHTTGVGAGEVISDPKILRMNVLKTFEVIDL 300  
DB 241 FKTQNNVAVLVDSIVDVIPLVDIVLNFHTTGVGAGEVISDPKILRMNVLKTFEVIDL 300  
QY 301 LSCLPYDVINAFFENVDEISLSFSLKAVRLRLGRVARKLDHYIEYGAAYLVLLVCVFG 360  
DB 301 LSCLPYDVINAFFENVDEISLSFSLKAVRLRLGRVARKLDHYIEYGAAYLVLLVCVFG 360  
QY 361 LGVAVARKLDHYIEYGAAYLVLLVCVGLAAMHMACIWSIGDYEFDEDTKTRNNSMY 420  
DB 361 LGVAVARKLDHYIEYGAAYLVLLVCVGLAAMHMACIWSIGDYEFDEDTKTRNNSMY 420  
QY 394 QLAMDIGTPYQFNCGSGKWEKGPSSKNVYISLSYFTMTSLTSVGFNGIAPSTDIETKIFA 453

```

DB 421 QIADIDTPIQFNGSGSGKMGEGSKNSVYISLYFTMTSLTSGVFGNIADSTDEKIFA 480
QY 454 VAIMIGSLIYATIFGNVTTIFQOMYANTNRYHEMLNSVRFLKLYQPKGISEVMYI 513
DB 481 VAIMIGSLIYATIFGNVTTIFQOMYANTNRYHEMLNSVRFLKLYQPKGISEVMYI 540
QY 514 VSTMWSRGIDTEKVLQICPKDMRADICVHLNRKVFKEHPAFRLASDGLRALAMEFQTV 573
DB 541 VSTMWSRGIDTEKVLQICPKDMRADICVHLNRKVFKEHPAFRLASDGLRALAMEFQTV 600
QY 574 HCAAGDILYHAGESVDSLCFVYSSLEYIQDDEVYAILGKGDVGVDVWKKEATLAQSCAN 633
DB 601 HCAAGDILYHAGESVDSLCFVYSSLEYIQDDEVYAILGKGDVGVDVWKKEATLAQSCAN 660
QY 634 VRALTYYDDLHVTKRDALOKVLEFYTAPSHSRNLLTYNLRKRIVFKRISDVKREER 693
DB 661 VRALTYYDDLHVTKRDALOKVLEFYTAPSHSRNLLTYNLRKRIVFKRISDVKREER 720
QY 694 MKRKNAPLILPDHPVRLRFQRFROQKEARLAAERGRDLDLDVEKGNVLTETHASANH 753
DB 721 MKRKNAPLILPDHPVRLRFQRFROQKEARLAAERGRDLDLDVEKGNVLTETHASANH 780
QY 754 SLVKASYVYVRESFATPVSEFOASTSGVVDHAKLQAPGSECLGPKGGGDCAKRRSMARF 813
DB 781 SLVKASYVYVRESFATPVSEFOASTSGVVDHAKLQAPGSECLGPKGGGDCAKRRSMARF 840
QY 814 KDCAGKSEDMNKVKASMETLPERTKASGEATLTKTDCSCGJTKSRLRLDNVGEASRP 873
DB 841 KDCAGKSEDMNKVKASMETLPERTKASGEATLTKTDCSCGJTKSRLRLDNVGEASRP 900
QY 874 QDRSPILAEVKSFPYPIPEOTLQATVLEVRHELEKEDIKALNAKMTNIEKQISEILRLITS 933
DB 901 QDRSPILAEVKSFPYPIPEOTLQATVLEVRHELEKEDIKALNAKMTNIEKQISEILRLITS 960
QY 934 RRSQSPOELFEISRPOSSESERDIFGAS 962
DB 961 RRSQSPOELFEISRPOSSESERDIFGAS 989

RESULT 3
ID 063472 PRELIMINARY; PRT; 962 AA.
AC 063472;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE POTASSIUM CHANNEL SUBUNIT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, CEREBELLUM;
RX MEDLINE=95009946; Pubmed=7925287;
RA Ludwig J., Terlau H., Wunder F., Brueggemann A., Pardo L.A.,
RA Marguardt A., Stuenkel W., Pongs O.;
RT "Functional expression of a rat homologue of the voltage gated ether
RT a go-go potassium channel reveals differences in selectivity and
RT activation kinetics between the Drosophila channel and its mammalian
RT counterpart.";
RL EMBL J.13:4451-4458(1994).
DR EMBL: Z34264; CAAB4018.1; .
DR InterPro: IPR000014; .
DR InterPro: IPR000595; .
DR InterPro: IPR000636; .
DR InterPro: IPR000700; .
DR InterPro: IPR001610; .
DR InterPro: IPR001622; .
DR InterPro: IPR002025; .
DR Pfam: PF00027; cNMP_binding; 1.
DR Pfam: PF00785; PAC; 1.

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DR Pfam: PF00914; CNG_membrane; 1.
DR PROSITE: PS50042; C_NMP_BINDING_3; 1.
DR SMART: SM00100; cNMP; 1.
DR Ionic channel.
SQ SEQUENCE 962 AA: 108290 MW: 69DFACE2DC435608 CRC64:

Query Match          97.8%; Score 4893; DB 11; Length 962;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 940; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTMAGGRGLVAPQNTFLENIVRSNDTNPVLGNAQIYMPPIYSNDGCKLSGYRAEY 60
DB 1 MTMAGGRGLVAPQNTFLENIVRSNDTNPVLGNAQIYMPPIYSNDGCKLSGYRAEY 60
QY 61 MOKSSCSFMVGEIDDKDIEKVRQFEYENMSFEILMYKKRTPVWFVFIAPIRNDO 120
DB 61 MOKSSCSFMVGEIDDKDIEKVRQFEYENMSFEILMYKKRTPVWFVFIAPIRNDO 120
QY 121 DKVVFELCTFSDITAFKQPIEDDSCGKMGKFAFLTALSSRGVLQOLAPSVQKGENVHK 180
DB 121 DKVVFELCTFSDITAFKQPIEDDSCGKMGKFAFLTALSSRGVLQOLAPSVQKGENVHK 180
QY 181 HSRLAEVLQSGDILPYKQKAPKTPPHILHYCYEKTWMDIILITFEYTAALVYVNS 240
DB 181 HSRLAEVLQSGDILPYKQKAPKTPPHILHYCYEKTWMDIILITFEYTAALVYVNS 240
QY 241 FETRONNNAWLVVDSIVDYIFLVYDVLNHTTFVGVAGEVISPKLIRNNYLKTWVIDL 300
DB 241 FETRONNNAWLVVDSIVDYIFLVYDVLNHTTFVGVAGEVISPKLIRNNYLKTWVIDL 300
QY 301 LSCLEVDYINAFENYDEGISLFSLSKVYRLRLGVARKLDBHYIEYGAVALVLYCVFG 360
DB 301 LSCLEVDYINAFENYDEGISLFSLSKVYRLRLGVARKLDBHYIEYGAVALVLYCVFG 360
QY 361 LAHMMACIWSYIGDYEIFDEDTKTLRNNSMLYOLAMDIGTPYQFNGSGSGKMGSPSKN 420
DB 361 LAHMMACIWSYIGDYEIFDEDTKTLRNNSMLYOLAMDIGTPYQFNGSGSGKMGSPSKN 420
QY 421 SVYISSLYFTMTSLTSGVGNIAPISTDIEKIFAVAIMIGSLIYATIFGNVTTIFQOMA 480
DB 421 SVYISSLYFTMTSLTSGVGNIAPISTDIEKIFAVAIMIGSLIYATIFGNVTTIFQOMA 480
QY 481 NTRNRYHEMLNSVRFLKLYQPKGISERYMDYIVSTMWSRGIDTEKVLQICPKDMRADI 540
DB 481 NTRNRYHEMLNSVRFLKLYQPKGISERYMDYIVSTMWSRGIDTEKVLQICPKDMRADI 540
QY 541 CVHLNRKVFKEHPAFRLASDGLRALAMEFQVHCAAGDILYHAGESVDSLCFVYSSGLE 600
DB 541 CVHLNRKVFKEHPAFRLASDGLRALAMEFQVHCAAGDILYHAGESVDSLCFVYSSGLE 600
QY 601 VIQDDEVYAILGKGDVGVDVWKKEATLAQSCANVRALTYCDLHVTKRDALOKVLEFYTA 660
DB 601 VIQDDEVYAILGKGDVGVDVWKKEATLAQSCANVRALTYCDLHVTKRDALOKVLEFYTA 660
QY 661 SHSFERNLILTYNLRKRIVFKRISDVKREERMKRKNAPLILPDHPVRLRFQRFROQ 720
DB 661 SHSFERNLILTYNLRKRIVFKRISDVKREERMKRKNAPLILPDHPVRLRFQRFROQ 720
QY 721 KEARLAERGGDLDLDVEKGNVLTETHASANHSLVKASYVYVRESFATPVSEFOASTSG 780
DB 721 KEARLAERGGDLDLDVEKGNVLTETHASANHSLVKASYVYVRESFATPVSEFOASTSG 780
QY 781 VPDHAKLQAPGSECLGPKGGGDCAKRRSMARFQKACGKSEDMNKVSKAESMETLPERTK 840
DB 781 VPDHAKLQAPGSECLGPKGGGDCAKRRSMARFQKACGKSEDMNKVSKAESMETLPERTK 840
QY 841 ASGEATLTKTDCSDGJTKSRLRLDNVGEASRPQDRSPILAEVKSFPYPIPEOTLQATV 900
DB 841 ASGEATLTKTDCSDGJTKSRLRLDNVGEASRPQDRSPILAEVKSFPYPIPEOTLQATV 900
QY 901 EYRHELEKEDIKALNAKMTNIEKQISEILRLSRSSQSPOELFEISRPOSSESERDIFG 960
DB 901 EYRHELEKEDIKALNAKMTNIEKQISEILRLSRSSQSPOELFEISRPOSSESERDIFG 960

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Db 901 EVKHEKEDIKALNAKMTSEIKOLSEILRIILMSRGSQSPDTCVSRPQSPESDRDIFG 960  
Qy 961 AS 962  
Db 961 AS 962

RESULT 4  
ID 018965 PRELIMINARY; PRT: 960 AA.  
AC 018965:  
DT 01-JAN-1998 (TREMblrel. 05, Created)  
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE EAG CHANNEL.  
GN EAG1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_Taxid=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Baumann A.;  
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y13430; CAAT3842.1; -.  
DR InterPro: IPR000014; -.  
DR InterPro: IPR000595; -.  
DR InterPro: IPR000636; -.  
DR InterPro: IPR000700; -.  
DR InterPro: IPR001610; -.  
DR InterPro: IPR001622; -.  
DR InterPro: IPR002025; -.  
DR Pfam: PF00027; cNMP\_binding; 1.  
DR Pfam: PF00785; PAC; 1.  
DR Pfam: PF00914; cNMP\_membrane; 1.  
DR PROSITE: PS50042; cNMP\_BINDING\_3; 1.  
DR SMART: SM00100; cNMP; 1.  
SQ SEQUENCE 960 AA; 108091 MW; 86FCD3303AE3B08 CRC64;

Query Match 96.8%; Score 4842; DB 6; Length 960;  
Best Local Similarity 96.8%; Pred. No. 0;  
Matches 931; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 MTMGGRGIVAPONTFLENTVRSNDNFVGNQIYDMPVYSNDGCKLSGYRABV 60  
Db 1 MTMGGRGIVAPONTFLENTVRSNDNFVGNQIYDMPVYSNDGCKLSGYRABV 60  
Qy 61 MOKSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKNRTPVWFEVKIAPIRNQ 120  
Db 61 MOKSTCSFMGELTDKDTIEKVRQTFENYEMNSFEILMYKKNRTPVWFEVKIAPIRNQ 120  
Qy 121 DKVVFELCTFSDITAFKQPIEDDSCCKGWGKFARLTRALTSRSGVLOQLAPSVQKGENVHK 180  
Db 121 DKVVFELCTFSDITAFKQPIEDDSCCKGWGKFARLTRALTSRSGVLOQLAPSVQKGENVHK 180  
Qy 181 HSRLAEVLOLGSDDLPOYKQKAPKPPHILHYCYFKTTWMDIILITLYTALVYVNS 240  
Db 181 HSRLAEVLOLGSDDLPOYKQKAPKPPHILHYCYFKTTWMDIILITLYTALVYVNS 240  
Qy 241 FKTRONNVAMLVDSIVIVIFLVLDIVLNFHTFVCPAGEVIDPDKLIRNNYKLTWFEVDL 300  
Db 241 FKTRONNVAMLVDSIVIVIFLVLDIVLNFHTFVCPAGEVIDPDKLIRNNYKLTWFEVDL 300  
Qy 301 LSCLEPYDVIAENVDGESSLSLKKVRLRLGLGVARKLDHYIEYGAIVLVLLCVFG 360  
Db 301 LSCLEPYDVIAENVDGESSLSLKKVRLRLGLGVARKLDHYIEYGAIVLVLLCVFG 360  
Qy 361 LAHHMNAICIVSICGYEIFDEDETKTIRNNSWLYQLAMDIGTYQFNGSSSGWEGSPSKN 420  
Db 361 LAHHMNAICIVSICGYEIFDEDETKTIRNNSWLYQLAMDIGTYQFNGSSSGWEGSPSKN 420

Qy 421 SVYISLFTYMTSLNSVSGNIAIPSTDIKIFAVAIMIGSLIATIFGVTTFIQQMYA 480  
Db 421 SVYISLFTYMTSLNSVSGNIAIPSTDIKIFAVAIMIGSLIATIFGVTTFIQQMYA 480  
Qy 481 NTRRYHEMLNSVDFLKLQVPRKGLSERVMDYIVSTWMSRGIDTFEVLQICKDRADI 540  
Db 481 NTRRYHEMLNSVDFLKLQVPRKGLSERVMDYIVSTWMSRGIDTFEVLQICKDRADI 540  
Qy 541 CVHLNRKVEKHPAFRLASDGLRALAMEFQYTHCAPGLDIYHAGESVDSLCEVSGSLE 600  
Db 541 CVHLNRKVEKHPAFRLASDGLRALAMEFQYTHCAPGLDIYHAGESVDSLCEVSGSLE 600  
Qy 601 VIODEVVAIILKGDFGVFWKEATLAOSCANVRLTYCDLHVIRDALQKYLEFTYAF 660  
Db 601 VIODEVVAIILKGDFGVFWKEATLAOSCANVRLTYCDLHVIRDALQKYLEFTYAF 660  
Qy 661 SHSESNLLITVNLKRIYPRKISDVKREBEERMKRNEAPLLPDPHVRRLFORPQQ 720  
Db 661 SHSESNLLITVNLKRIYPRKISDVKREBEERMKRNEAPLLPDPHVRRLFORPQQ 720  
Qy 721 KEARLAERGRDLDLDVEKGNVLETHASANSILKASVYTVRESPAPVFOASTSG 780  
Db 721 KEARLAERGRDLDLDVEKGNVLETHASANSILKASVYTVRESPAPVFOASTSG 780  
Qy 781 VPDHAKLQAPGSECLQPKGGGDCAKRKSWARFKDAGCKSEDNKKVSKAEMETLPERTK 840  
Db 781 VPDHAKLQAPGAGGLQPKGGGDCAKRKSWARFKDAGCKSEDNKKVSKAEMETLPERTK 840  
Qy 841 ASGEATLKKTDCSDGSLTTSKDLRLDNVGEARSPQDASPLAEVKKHSPYPIPEOTLQAVL 900  
Db 841 ASGEATLKKTDCSDGSLTTSKDLRLDNVGEARSPQDASPLAEVKKHSPYPIPEOTLQAVL 900  
Qy 901 EVKHEKEDIKALNAKMTSEIKOLSEILRIILTSRRSSSQPOELFEISRPQSPESDRDIFG 960  
Db 901 EVKHEKEDIKALNAKMTSEIKOLSEILRIILTSRRSSSQPOELFEISRPQSPESDRDIFG 960  
Qy 961 AS 962  
Db 961 AS 962

RESULT 5  
ID 060603 PRELIMINARY; PRT: 989 AA.  
AC 060603:  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE LONG (ELECTOCARDIOGRAPHIC) QT SYNDROME 2 (POTASSIUM CHANNEL SUBUNIT).  
GN KCNH1 OR IOT2 OR M-EAG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=WHOLE BRAIN;  
RX MEDLINE=94211879; PubMed=8159766;  
RA Warneke J.W., Ganetzky B.;  
RT "A family of potassium channel genes related to eag in Drosophila and mammals."  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).  
DR EMBL; U04294; AAA62474.1; -.  
DR MGD; MGI:1341721; Kcnhl.  
DR InterPro: IPR000014; -.  
DR InterPro: IPR000595; -.  
DR InterPro: IPR000636; -.  
DR InterPro: IPR000700; -.  
DR InterPro: IPR001610; -.  
DR InterPro: IPR001622; -.  
DR InterPro: IPR002025; -.  
DR Pfam: PF00027; cNMP\_binding; 1.  
DR Pfam: PF00785; PAC; 1.

DR Pfam: PF00914; CNG\_membrane; 1.  
 DR PROSITE: PS50042; CNGP\_BINDING\_3; 1.  
 DR SMART: SM00100; CNGP; 1.  
 KW Ionic channel.  
 SO SEQUENCE 989 AA; 111313 MW; BA9B8C30F958CDA CRC64;

Query Match 96.5%; Score 4824.5; DB 11; Length 989;  
 Best Local Similarity 94.3%; Pred. No. 0;  
 Matches 933; Conservative 10; Mismatches 19; Indels 27; Gaps 1.

QY 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPIYVSDGFCCKLSGHRAEV 60  
 DB 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPIYVSDGFCCKLSGHRAEV 60  
 QY 61 MOKSTGSPMGELTDKDTIEKVRQTFENYEMNSPEILMYKKNRPPVWFVKIAPIRNEQ 120  
 DB 61 MOKSTGSPMGELTDKDTIEKVRQTFENYEMNSPEILMYKKNRPPVWFVKIAPIRNEQ 120  
 QY 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 DB 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 QY 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 DB 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 QY 181 HSRLAEVLQSGDILPQYKQKAPKTPPHIILHYCVFKTTWMIILITFYTAIIVPYNVS 240  
 DB 181 HSRLAEVLQSGDILPQYKQKAPKTPPHIILHYCVFKTTWMIILITFYTAIIVPYNVS 240  
 QY 241 FKTRONNVAMLVDSIVDVIPLVDIVLNFHTTFVGPAGEVISDPKILRNMYLKTWFEIDL 300  
 DB 241 FKTRONNVAMLVDSIVDVIPLVDIVLNFHTTFVGPAGEVISDPKILRNMYLKTWFEIDL 300  
 QY 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 DB 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 QY 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 DB 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 QY 334 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 393  
 DB 334 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 393  
 QY 361 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 420  
 DB 361 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 420  
 QY 394 OLAMDITPQFONGSGSGKMGKSPKSNVYSSLYFTMTSLTSGVFGNIASTIDEKFEA 453  
 DB 421 OLAMDITPQFONGSGSGKMGKSPKSNVYSSLYFTMTSLTSGVFGNIASTIDEKFEA 480  
 QY 454 VALIMIGSLYATFFGVNTTTFQOMYANTNRYHEMLNSVRFELKYQVPKGISERVMYI 513  
 DB 481 VALIMIGSLYATFFGVNTTTFQOMYANTNRYHEMLNSVRFELKYQVPKGISERVMYI 540  
 QY 514 VSTWMSRGIDTEKVLQICPKMRADICVHLNRKVFKEHPAFRLASDGLALAMEFQTV 573  
 DB 541 VSTWMSRGIDTEKVLQICPKMRADICVHLNRKVFKEHPAFRLASDGLALAMEFQTV 600  
 QY 574 HCAPBGDIYHAGESVDSLCFYVSGSLEYIODEVVAIIGKDDVGFVFWKATIAQSCAN 633  
 DB 601 HCAPBGDIYHAGESVDSLCFYVSGSLEYIODEVVAIIGKDDVGFVFWKATIAQSCAN 660  
 QY 634 VRALTYCDLHVIRKDAQVLEFYTAFSHFSRNLILTYNKRRIYFKISDVAREEER 693  
 DB 661 VRALTYCDLHVIRKDAQVLEFYTAFSHFSRNLILTYNKRRIYFKISDVAREEER 720  
 QY 694 MKRKNRAPLILPDHPVRLQFRROQKEARLAAERGRDLDDLVEKGNVLTTHASANH 753  
 DB 721 MKRKNRAPLILPDHPVRLQFRROQKEARLAAERGRDLDDLVEKGNVLTTHASANH 780  
 QY 754 SLVKASYVYRESPATVFSQASTSCVPHAKIQAAPGSECLGPKGGGCAKRRSWARF 813  
 DB 781 SLVKASYVYRESPATVFSQASTSCVPHAKIQAAPGSECLGPKGGGCAKRRSWARF 840  
 QY 814 KDACGRKEDNNKYSKASMETLPERTKASGATLKTDSOSGTTKSLRLDNNGEARSP 873  
 DB 841 KDACGRKEDNNKYSKASMETLPERTKASGATLKTDSOSGTTKSLRLDNNGEARSP 900  
 QY 874 QDSPLIAEVKHSFYPIPEOTLQATVLEVRHELKEDIKALNAKNTNIEKOLSEILRITS 933  
 DB 874 QDSPLIAEVKHSFYPIPEOTLQATVLEVRHELKEDIKALNAKNTNIEKOLSEILRITS 933

DB 901 QDRSPILAEVKSFPYPIPEOTLQATVLEVRHELKEDIKALNAKNTNIEKOLSEILRITS 960  
 QY 934 RRSOSPOELFEISRPOSPESERDIFGAS 962  
 DB 961 RRSOSPOELFEISRPOSPESERDIFGAS 989

RESULT 6  
 ID 018966 PRELIMINARY; PRT: 987 AA.  
 AC 018966.  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE EAG CHANNEL.  
 GN EAG3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Baumann A.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y13431; CAA73843.1; -;  
 DR InterPro: IPR000014; -;  
 DR InterPro: IPR000595; -;  
 DR InterPro: IPR000636; -;  
 DR InterPro: IPR000700; -;  
 DR InterPro: IPR001610; -;  
 DR InterPro: IPR001622; -;  
 DR InterPro: IPR002025; -;  
 DR Pfam: PF00027; CNGP\_binding; 1.  
 DR Pfam: PF00785; PAC; 1.  
 DR Pfam: PF00914; CNG\_membrane; 1.  
 DR PROSITE: PS50042; CNGP\_BINDING\_3; 1.  
 DR SMART: SM00100; CNGP; 1.  
 SO SEQUENCE 987 AA; 110917 MW; 0BF9FB866297DCAF CRC64;

Query Match 96.4%; Score 4818.5; DB 6; Length 987;  
 Best Local Similarity 94.1%; Pred. No. 0;  
 Matches 931; Conservative 15; Mismatches 14; Indels 29; Gaps 2;

QY 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPIYVSDGFCCKLSGHRAEV 60  
 DB 1 MTMAGGRGLVAPONTFLENIVRSNDTNFVLGNAQIVDMPIYVSDGFCCKLSGHRAEV 60  
 QY 61 MOKSTGSPMGELTDKDTIEKVRQTFENYEMNSPEILMYKKNRPPVWFVKIAPIRNEQ 120  
 DB 61 MOKSTGSPMGELTDKDTIEKVRQTFENYEMNSPEILMYKKNRPPVWFVKIAPIRNEQ 120  
 QY 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 DB 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 QY 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 DB 121 DKVVLFLCTFSIDITAFKQPIEDDSCGKMGKFAFLTRALTSRGVLOQLAPSVQKGENVHK 180  
 QY 181 HSRLAEVLQSGDILPQYKQKAPKTPPHIILHYCVFKTTWMIILITFYTAIIVPYNVS 240  
 DB 181 HSRLAEVLQSGDILPQYKQKAPKTPPHIILHYCVFKTTWMIILITFYTAIIVPYNVS 240  
 QY 241 FKTRONNVAMLVDSIVDVIPLVDIVLNFHTTFVGPAGEVISDPKILRNMYLKTWFEIDL 300  
 DB 241 FKTRONNVAMLVDSIVDVIPLVDIVLNFHTTFVGPAGEVISDPKILRNMYLKTWFEIDL 300  
 QY 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 DB 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 QY 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 DB 301 LSCLPYDVINAFAENVD-----GISLSFSSLSKVVRLR 333  
 QY 334 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 393  
 DB 334 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 393  
 QY 361 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 420  
 DB 361 LGRVARKLDHYIEYGAVALVLCVFGSLAHHMACIWSIGDYEIFDEDEDTKIRNNSWLY 420



DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
 DE POTASIIUM CHANNEL EAG2.  
 GN  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 OC Mammalia: Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAUE-DAWLEY;  
 RX MEDLINE=20063035; Pubmed=10594062;  
 RA Saganich M.J., Vega-Saenz de Miera E., Nadal M.S., Baker H.,  
 RA Coetzee W.A., Rudy B.;  
 RT "Cloning of components of a novel subthreshold-activating K<sup>+</sup> channel  
 RT with a unique pattern of expression in the cerebral cortex."  
 RL J. Neurosci. 19:10789-10802(1999).  
 DR EMBL: AF185637; AAF19354.1; -.  
 DR InterPro: IPR000595; -.  
 DR InterPro: IPR000636; -.  
 DR InterPro: IPR000700; -.  
 DR InterPro: IPR001610; -.  
 DR InterPro: IPR001622; -.  
 DR InterPro: IPR002025; -.  
 DR Pfam: PF00027; CNMP-binding; 1.  
 DR Pfam: PF00785; PAC; 1.  
 DR Pfam: PF00914; CNG-membrane; 1.  
 DR PROSITE: PS50042; CNMP-BINDING\_3; 1.  
 DR SMART: SM00100; CNMP; 1.  
 SQ SEQUENCE 988 AA; 111928 MW; 7C9F1338FC08F7ED CRC64;

Query Match 75.3%; Score 3767.5; DB 11; Length 988;  
 Best Local Similarity 73.0%; Pred. No. 2,2e-274;  
 Matches 728; Conservative 100; Mismatches 114; Indels 55; Gaps 13;

QY 3 MAGGRGLVAPONTLENIYRSNDINEVLGMAQIVDMPYVSDGCKLSGYHAEVQ 62  
 1 MPGGRGLVAPONTLENIYRSSESEFLGNAQIVDMPYVSDGCKLSGYHAEVQ 60  
 DB 1 MPGGRGLVAPONTLENIYRSSESEFLGNAQIVDMPYVSDGCKLSGYHAEVQ 60

QY 63 KSSYCSMYGELTDKTIIEKYRQTFEYEMNSFEILMKKRTVWFFVKIAPIRNEDK 122  
 61 KSSYCSMYGELTDKTIIEKYRQTFEYEMNSFEILMKKRTVWFFVKIAPIRNEDK 120  
 DB 61 KSSYCSMYGELTDKTIIEKYRQTFEYEMNSFEILMKKRTVWFFVKIAPIRNEDK 120

QY 123 VVFLCFEFSITAFKPIEDDSCKMGKFAFLTRALNSSRGVLOQLAPSVCKGNVHHS 182  
 121 VVFLCFEFSITAFKPIEDDSCKMGKFAFLTRALNSSRGVLOQLAPSVCKGNVHHS 179  
 DB 121 VVFLCFEFSITAFKPIEDDSCKMGKFAFLTRALNSSRGVLOQLAPSVCKGNVHHS 179

QY 183 RLAEVLQSGDILPOYKQEAAPKPPHILHCVKFTTMDIILTFETALIPVNSFK 242  
 180 RLAEVLQSGDILPOYKQEAAPKPPHILHCVKFTTMDIILTFETALIPVNSFK 239  
 DB 180 RLAEVLQSGDILPOYKQEAAPKPPHILHCVKFTTMDIILTFETALIPVNSFK 239

QY 243 TRONNVAWLVDSDIVLVDVILNFTFFVAGAVISDPKILRMNYLKTWVIDLS 302  
 240 TKONNVAWLVDSDIVLVDVILNFTFFVAGAVISDPKILRMNYLKTWVIDLS 299  
 DB 240 TKONNVAWLVDSDIVLVDVILNFTFFVAGAVISDPKILRMNYLKTWVIDLS 299

QY 303 CLPYDVINAENDEGSSLSFSLKVVRLRLRGVARKLDHYTRYGAIVLVLCVSGLA 362  
 300 CLPYDVINAENDEGSSLSFSLKVVRLRLRGVARKLDHYTRYGAIVLVLCVSGLA 359  
 DB 300 CLPYDVINAENDEGSSLSFSLKVVRLRLRGVARKLDHYTRYGAIVLVLCVSGLA 359

QY 363 AHMMACIWSYIGDEYFEDETKTRNNMSLYOLAMDIGTFPOFGSSGKEGPKRSKV 422  
 360 AHMMACIWSYIGDEYFEDETKTRNNMSLYOLAMDIGTFPOFGSSGKEGPKRSKV 418  
 DB 360 AHMMACIWSYIGDEYFEDETKTRNNMSLYOLAMDIGTFPOFGSSGKEGPKRSKV 418

QY 423 YISLXFTMTSLTSVFGNIAPTSDIEKIFAVAIMIGSLYATIFGNVTTIFPOOMANT 482  
 419 YISLXFTMTSLTSVFGNIAPTSDIEKIFAVAIMIGSLYATIFGNVTTIFPOOMANT 478  
 DB 419 YISLXFTMTSLTSVFGNIAPTSDIEKIFAVAIMIGSLYATIFGNVTTIFPOOMANT 478

QY 483 NRHEMLNVRDLKLYOVKGLSERVMDYIVSTWSKRGIDTEKYLQICPKDRADICV 542  
 479 NRHEMLNVRDLKLYOVKGLSERVMDYIVSTWSKRGIDTEKYLQICPKDRADICV 538  
 DB 479 NRHEMLNVRDLKLYOVKGLSERVMDYIVSTWSKRGIDTEKYLQICPKDRADICV 538

QY 543 HLNKRVKEHPARFLASDGLRALAMEFQVHCARGLIYHAGSVSLCFVSGSLEVI 602  
 543 HLNKRVKEHPARFLASDGLRALAMEFQVHCARGLIYHAGSVSLCFVSGSLEVI 602  
 DB 543 HLNKRVKEHPARFLASDGLRALAMEFQVHCARGLIYHAGSVSLCFVSGSLEVI 602

DB 539 HLNKRVKEHPARFLASDGLRALAMEFQVHCARGLIYHAGSVSLCFVSGSLEVI 598  
 QY 603 QDEEVVAIIGKGVDFGVFMKEATLAQSCANRALTYYCDLHYKRDALQVLEFYAFSH 662  
 DB 599 QDEEVVAIIGKGVDFGVFMKEATLAQSCANRALTYYCDLHYKRDALQVLEFYAFSH 658  
 QY 663 SFSRNLITLYNLRKRIVFRKISDVAKREEERMKRKNAPLIPDPHVRRLFORFROKE 722  
 DB 659 SFSRNLITLYNLRKRIVFRKISDVAKREEERMKRKNAPLIPDPHVRRLFORFROKE 718

QY 723 ARLAERGRDIDDDLVKGNVLEHASNH--SLYKASVYVYRESPATPVFOASTSG 780  
 DB 719 LR--NQSASQSDP---ERSQLOVESRPLQNGASINGTSVTV--SQIRPQ---TSLAP 767

QY 781 VPDHAKIAPGSECLGPKGGG---DCAK-----RKSMAFKACG---KSPD 822  
 DB 768 VPDHAKIAPGSECLGPKGGG---DCAK-----RKSMAFKACG---KSPD 822

QY 823 WNKVKAESMETLPPRTKASGEAT-----LKTSDSCDGIKSDRLDNVGEARSPODR 876  
 DB 828 WNKVKAESMETLPPRTKASGEAT-----LKTSDSCDGIKSDRLDNVGEARSPODR 887

QY 877 SPILAEVKSHPYPIPBQTLQATVLEHBELEKEDIKALNAKMTNEKQSLILTLTSR-- 934  
 DB 888 SPILAEVKSHPYPIPBQTLQATVLEHBELEKEDIKALNAKMTNEKQSLILTLTSR-- 947

QY 935 --RSSQSP-----QELFELSPQSPESND 957  
 DB 948 POTSPPKQPIPLQVPPQIPPCODIFSVSPESPSDKD 984

RESULT 9  
 Q9VXZ6 PRELIMINARY; PRT: 1174 AA.  
 AC Q9VXZ6;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE EAG PROTEIN.  
 GN EAG OR CG10952.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:  
 OC Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha;  
 OC Ephydroidea: Drosophilidae: Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; Pubmed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Blaise J.R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brothstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Chertis J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dudin K.J., Evangelista C.C., Ferrara C., Fertiera S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwan C.,  
 RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,





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QY 3 MAGGRGLVAPONTFLENIVRSN--DTNEVLGNAQIVDMPVYNSDGFCKLSGYHRAEV 60
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MPVGRGLVAPONTFLENIVRSNADTSFLANQVVDYPIYVNCDSKLVGTRAEI 60
QY 61 MOKSSTCSFMGELTDKOTIEKVFOTFENYEMNSFEILMKKRRTPVFEVKIAPIRNEQ 120
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MOKPCLSLAFMGEHGEVSLQKMOEALNARTQOAEIGCKKKNKTPIMLLVHLAPIKNHK 120
QY 121 DKVYFLCTFSOTAFKOPTEEDSCGKGFARLFRALTSNGVLAQOLAPSVQKGENVHK 180
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DAVVLYLCOFDTPLKQPLDENNKGSRLIQIAR-TAKSKQGFNQI-----ETKDLK 174
QY 181 -----HSRLAEVLAQSDILPOYKOEAKTPPHILHYCVFKTWMILITFYTAIY 235
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 SPQNTSSNPNQVNMNGGMLPOYROETPKTSPIILHYSFETIMDSILALTFYTAEV 234
QY 236 PYNVSEK-----TRQN-----NVAMLVDSIVDVIPLVDIVLNFHTFVGPAGE 279
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 PNLIAFKNSLRPFYLLISRENGGIDSYA--LMDSIVDVIFPADILLNFHTFVGPAGE 292
QY 280 VISDPKLRMYLTKWFIYDILSCLPYDINAFENVDEGISLSLKYVRLRIGRVAR 339
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 VVIEPSVIRQNFESKWFLLDLSCLPYDI FYWFKRDERIGSLFSALKVYLLRIGRVAR 352
QY 340 KLDHYIEGAIVLYLVCVGLAAHMACIWSIGDYEIFDEDTKTIRNSMLYOLAMDI 399
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 KLDNLEGAITLLLLCAVYVAHMLACVFWIGDSEVRLKMDNALPDGMLKMSLDL 412
QY 400 GTPYQFNGSGGKMGSPKNSVYISLYFTMTSLTSVGFNIAPSTDIKIFAVAIMI 459
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 ROHYNIPLSNKTTLVGGPSRTSAYISLYTWSGMSVGFNIASNTDEKIFGVCMMI 472
QY 460 GSLYATIFGAVTTTFQOMYANTNRYHEMLNSVRDLKLYOVPKGLSEVMDIYVSTSM 519
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 SALLYAALFGHMTTIIQOMTSYVYHSMISVREFIKLOEIPKELAEVMDYVSTWVM 532
QY 520 SRGIDTEVLQICPKMDADICVHLNRKVFKEHPAFRLASDGLRALMEPOTVCAPE 579
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 533 TKGIDTAKVLYGCPKMDADICVHLNRKVFKEHSCFRLASDGLSLAFLELNLNAAPD 592
QY 580 LIYHAGESVDSLCFVSGSLEYIDDEVVALIGKGVDFGVFWK--EATLAQSCANVRLT 638
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 593 LLYHGESVDALMFVYSSLEYIDDEVVALIGKGVDFGVFWK--EATLAQSCANVRLT 652
QY 639 YCDLHVIRKDALQVLEYTAFSHSFNRLLITVNLRRRIYFRKISDVKREEBERKRN 698
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 653 YSDLMIKKDKLMDVLDYFKAFANSPARNMTLTYNLTRHMKFRKYADVAREKELDAKRN 712
QY 699 EAPLILPDHVRRLFORFROCKEARLAEKGRDLDDLQVFKG---AVLTTHASANS 755
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 713 E-KLTPNDHDIRKLLEFMRREHGRIPSP---MFADIEIGLKKSTEISRISSLSHM 766
QY 756 V-----KASVYVRESPTPVSFQASTSGVPDHAQLQAPSECLCPKGGGCAKRR 808
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 767 IDENGSGSSVYKSPKRPKRPMLKROTVD-----EDALST 804
QY 809 SWAREKDACGSEDMNWKYKASMETLPERTKASEATLKTDCSDSGITKSD-LRLDNV 867
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 805 SMGMDK---KDEWSSLSNITK--EMKSKFDIIG-RLTIEIQNSRLALLERVLIGN 857
QY 868 GEAKSPQ-----DASPLIAEYKHSFYPLPEOTLQATVLEVR 903
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 858 GGANTPTMPYGSFALSNGRLTLDAAPVARSVMSBOHPHMQRTSTVPEPLR 912

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DE HYPOTHETICAL 105.5 KDA PROTEIN F16B3.1 IN CHROMOSOME IV.
GN F16B3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCB1_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Kemp K.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036955; AAB88348.1; -.
DR WormBep; F16B3.1; CE24905.
DR InterPro; IPR000014; -.
DR InterPro; IPR000595; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR000700; -.
DR InterPro; IPR001610; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR002016; -.
DR InterPro; IPR002025; -.
DR Pfam; PF00027; cAMP_binding; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00914; CNG_membrane; 1.
DR PROSITE; PS50042; cAMP_BINDING_3; 1.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR SMART; SM00100; cAMP; 1.
DR Hypothetical protein.
SQ SEQUENCE 934 AA; 105476 MW; 04459EFACB009A5 CRC64;

Query Match 44.5%; Score 2226.5; DB 5; Length 934;
Best Local Similarity 52.6%; Pred. No. 1.5e-158;
Matches 447; Conservative 132; Mismatches 194; Indels 77; Gaps 14;

QY 3 MAGGRGLVAPONTFLENIVRSN--DTNEVLGNAQIVDMPVYNSDGFCKLSGYHRAEV 60
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Db 1 MPVGRGLVAPONTFLENIVRSNADTSFLANQVVDYPIYVNCDSKLVGTRAEI 60
QY 61 MOKSSTCSFMGELTDKOTIEKVFOTFENYEMNSFEILMKKRRTPVFEVKIAPIRNEQ 120
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MOKPCLSLAFMGEHGEVSLQKMOEALNARTQOAEIGCKKKNKTPIMLLVHLAPIKNHK 120
QY 121 DKVYFLCTFSOTAFKOPTEEDSCGKGFARLFRALTSNGVLAQOLAPSVQKGENVHK 180
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DAVVLYLCOFDTPLKQPLDENNKGSRLIQIAR-TAKSKQGFNQI-----ETKDLK 174
QY 181 -----HSRLAEVLAQSDILPOYKOEAKTPPHILHYCVFKTWMILITFYTAIY 235
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 SPQNTSSNPNQVNMNGGMLPOYROETPKTSPIILHYSFETIMDSILALTFYTAEV 234
QY 236 PYNVSEK-----TRQN-----NVAMLVDSIVDVIPLVDIVLNFHTFVGPAGE 279
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 PNLIAFKNSLRPFYLLISRENGGIDSYA--LMDSIVDVIFPADILLNFHTFVGPAGE 292
QY 280 VISDPKLRMYLTKWFIYDILSCLPYDINAFENVDEGISLSLKYVRLRIGRVAR 339
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 VVIEPSVIRQNFESKWFLLDLSCLPYDI FYWFKRDERIGSLFSALKVYLLRIGRVAR 352
QY 340 KLDHYIEGAIVLYLVCVGLAAHMACIWSIGDYEIFDEDTKTIRNSMLYOLAMDI 399
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 KLDNLEGAITLLLLCAVYVAHMLACVFWIGDSEVRLKMDNALPDGMLKMSLDL 412
QY 400 GTPYQFNGSGGKMGSPKNSVYISLYFTMTSLTSVGFNIAPSTDIKIFAVAIMI 459
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 ROHYNIPLSNKTTLVGGPSRTSAYISLYTWSGMSVGFNIASNTDEKIFGVCMMI 472
QY 460 GSLYATIFGAVTTTFQOMYANTNRYHEMLNSVRDLKLYOVPKGLSEVMDIYVSTSM 519
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 SALLYAALFGHMTTIIQOMTSYVYHSMISVREFIKLOEIPKELAEVMDYVSTWVM 532
QY 520 SRGIDTEVLQICPKMDADICVHLNRKVFKEHPAFRLASDGLRALMEPOTVCAPE 579
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Db 533 TKGIDTAKVLYGCPKMDADICVHLNRKVFKEHSCFRLASDGLSLAFLELNLNAAPD 592
QY 580 LIYHAGESVDSLCFVSGSLEYIDDEVVALIGKGVDFGVFWK--EATLAQSCANVRLT 638
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Db 593 LLYHGESVDALMFVYSSLEYIDDEVVALIGKGVDFGVFWK--EATLAQSCANVRLT 652
QY 639 YCDLHVIRKDALQVLEYTAFSHSFNRLLITVNLRRRIYFRKISDVKREEBERKRN 698
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Db 653 YSDLMIKKDKLMDVLDYFKAFANSPARNMTLTYNLTRHMKFRKYADVAREKELDAKRN 712
QY 699 EAPLILPDHVRRLFORFROCKEARLAEKGRDLDDLQVFKG---AVLTTHASANS 755
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 713 E-KLTPNDHDIRKLLEFMRREHGRIPSP---MFADIEIGLKKSTEISRISSLSHM 766
QY 756 V-----KASVYVRESPTPVSFQASTSGVPDHAQLQAPSECLCPKGGGCAKRR 808
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 767 IDENGSGSSVYKSPKRPKRPMLKROTVD-----EDALST 804
QY 809 SWAREKDACGSEDMNWKYKASMETLPERTKASEATLKTDCSDSGITKSD-LRLDNV 867
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 805 SMGMDK---KDEWSSLSNITK--EMKSKFDIIG-RLTIEIQNSRLALLERVLIGN 857
QY 868 GEAKSPQ-----DASPLIAEYKHSFYPLPEOTLQATVLEVR 903
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 858 GGANTPTMPYGSFALSNGRLTLDAAPVARSVMSBOHPHMQRTSTVPEPLR 912

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Db 517 PRDMKADICVHLNKRKVENHSCFRLASDGLSLAMFLELNHNAERDLYHTGESVDALM 576
Oy 593 FVSGSLEVIODDEVYAILGKGDVFGDVMK-EATLAOSCANVRLTYCDLHVIRKDALQ 651
Db 577 FVSGSLEVIODDEVYAILGKGDVFGDVMKANGSTGSAANVRLTYSDLHKIKDKLXLM 636
Oy 653 KYLEEYTAFSHFSRNLITYNLKRRIYVKISDVAKREEEMKKRKNAPLLIPDPHVR 711
Db 637 DVLDDYKAFANSPARNMTLYNLTHRMKFRKAVADYKREKELAKRKN-KLTLPHNDHPTR 695
Oy 712 RLFOFRFOOKEARLAEGRDLDDLDEKGG---NYLTHEASANSILV-----KASVY 761
Db 696 KLFPMREKREHGRIPTSP-----MPADIEKGLKSTETISRISLSHSMIDETGGGSSYVK 750
Oy 762 TVRESPPATPVFSQAASSTGVPDPAKLAQAPGSECLGPKGGGDCAKRRKSWAREKACGKE 821
Db 751 SPRSKPRKPRPLMKRQTVD-----EDALSTSMGMK-----KOR 784
Oy 822 DMNKYSKAES 831
Db 785 EWSLSLNIXT 794

RESULT 12
Oy 054853 PRELIMINARY; PRT; 950 AA.
AC 054853;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE POTASSIUM CHANNEL.
GN ERG2.
OC Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi W., Wymore R.S., Wang H.-S., Pan Z., Cohen I.S., McKinnon D.,
RA Dixon J.E.;
RL J. Neurosci. 0:0-0(1997).
DR EMBL, AF016192; AAB94742.1; -.
DR InterPro: IPR000595; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001610; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002025; -.
DR Pfam: PF00027; CNMP_binding; 1.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00914; CNM_membrane; 1.
DR ProSITE, PS50042; CNMP_BINDING_3; 1.
DR SMART, SM00100; CNMP; 1.
KW Ionic channel.
SQ SEQUENCE 950 AA: 105705 MW: ABA5674B08776F0 CRC64;

Query Match 29.4%; Score 1471.5; DB 11; Length 950;
Best Local Similarity 40.9%; Pred. No. 9,5e-102;
Matches 296; Conservative 143; Mismatches 218; Indels 67; Gaps 11;

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Db 184 FTLNEVEPNLEKHSRSTETIELIAPHKVERQNTTE-KVQVLSLGDVLPETKLOA 241
Oy 203 KTRPHIILHLCVFKTTMDWIIILTFETAILVPYNSF-----KTRONVNW-----L 251
Db 242 PRHRCGTILHSPPKAWMDLILLIYITAVFTPYSAFLISNODSQRCTGCTGSPLT 301
Oy 252 VDSIVDVIFLVDIVLNFHTFVGPAGEVISDPKLRIMNYLKTWFDLISCLPYDVINA 311
Db 302 VVDIIVIMFVDIVLINFRTYVNTDEVVSHPRRIAVHVEFKGMFLIDVAAIPDLL-I 360
Oy 312 FENVDCISSLSLAVVRLRLGRVARKDHYIEGAANVLVLVCFGLAHMAMCIWY 371
Db 361 FRTSDSETTLLIGLTKTARLRLVRAARKIDRYSXGAANVFLMLCFALIAHMLCWIY 420
Oy 372 SIDVEIFEDETKTIRNNSLQOLAMDIGTPYONGSGSGSKGPKNSVYISLSTFTM 431
Db 421 AIGNVERPYLEPKI-----GMLDSLGAOLGR--QYNSDPA---SGPSVDKVTALYFTF 471
Oy 432 TSLTSVGFNIAPSTDIKIFAVAIMIGSLYATYFGVNTYTFQDMYANTNRYHEMLNS 491
Db 472 SLSLVGFQNVSPNTNSEKVFSCVMILGSLMVASIFGNVSAIIQLRYSGTARHTQMLR 531
Oy 492 VDFPLKLYOVPKGLSERWMDYIVSTWSMSRGIDTEKYLQICPKDMRADICVHLNKRKVE 551
Db 532 VKEFIFRHOIIPNPLRORLIEYFQHAWSYTNGIDIMNAVILKGFPCIDADICLHLRALQH 591
Oy 552 HPAFRLASDGLRALMEPOTVHCAPGDLTYHAGESVDISLCPVSGSLEVIODDEVYAIL 611
Db 592 CPARFGASKCLRALVAKFFTHAPGDTLVHLGSDVSLTFISRGSIELRLDDVYAIL 651
Oy 612 GKGDVFGDVMFKATLAOSCANVRLTYCDLHVIRKDALQKLEFYAFSFSRNLILT 671
Db 652 GRKNDIGEPASLIARPKSSADVRLTYCDLHKIRRADLEVDIMYAFADFTMNKLEVT 711
Oy 672 YNLR 675
Db 712 FNLR 715

RESULT 13
Oy 09H252 PRELIMINARY; PRT; 994 AA.
AC 09H252;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE EAG-RELATED GENE MEMBER 2.
GN ERG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Titus S.A., Ganetzkv B.S.;
RA Submitted (OCT-2000) to the EMBL/GenBank/DBD databases.
DR EMBL, AF311913; AAG40871.1; -.
SQ SEQUENCE 994 AA: 109924 MW: BE9ECB349A798576 CRC64;

Query Match 29.4%; Score 1468.5; DB 4; Length 994;
Best Local Similarity 41.0%; Pred. No. 1,7e-101;
Matches 297; Conservative 141; Mismatches 219; Indels 67; Gaps 11;

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Oy 125 LFLCTFSDITAFKOPIEDDSCK-----GMGKFA-----152
Db 124 MFIINFEEDLAOLAKCSRSLSORLLSOSFLGSECSHGPGPGPGTGKRTTISQIPQ 183
Oy 153 -----RLTRALTSNGVLOQLAPS--VOKGENVHKSRLAEVLOQLSDLPQKOA 202
Db 184 FTLNFEENFEKHSSTTEIEIAPKRVKVERTONVTE--KVTOVLSGADVLPEYKLOA 241
Oy 203 PKTPPHIILHCYCFKFTWMDWIIILTFYATILVPAVNSF-----KTQONNVAM-----L 251
Db 242 PRIRKRWITLHSPKAWMDLILLYITTAFTYSAAFLLSDODESRGACSTYCSPLT 301
Oy 252 VQDSIVDVILVILVILNFTTFVPAGEVISDPKILRNMYLKTWVIDLLSCLPYVINA 311
Db 302 VVDLIVDMIEVDIVINRTTYVMTNDEVSHPRILAVHYKGMFLDMVAAPDL-L 360
Oy 312 FENVDEGISLFSKLVYRLRLGKRVARKLDHYLEYGAVALVLCVFGLAHMACTIY 371
Db 361 FRTGSDETTYLIGLTKTARLRLRVARAKLDYSEYGAVALFLMCTFALLAHMTACTIY 420
Oy 372 SIGYEIPEDETKTIRNNSMILYOLAMDIGTPYQFNGSGSGKWEKGSNSVYISLFTM 431
Db 421 AIGNVERPYLEHKT-----GWLDSLGVOIGKRY--NGSDPA---SGPSVQDKYVATLYEFT 471
Oy 432 TSLTSVGFGNIAFSTDEKIPAVAIMIGSLIYATIFGNMTTIFQOMYANTNRHYHEMLNS 491
Db 472 SLSLTSVGFGNISPMNTNSKRVFSICVMLIGSLMVASIFGNVSAIIQRLXSGTARITQMLR 531
Oy 492 VRDFLKYQVPGKLSERVMDYIVSTWSKRGIDTEKVLQICPKDMRADICVHLNRKVEKE 551
Db 532 VKERIRFHQJPNPLRQRLSEYFOHAMSTYNGIDMNAVLKGPCELOADICHLHALLQ 591
Oy 552 HPARLASDGLRLALAMEFQVHCAFGDLIYHAGESVDSLFPVYSGSELEVODDEVAAIL 611
Db 592 CPASGAGKGGKLRALAVKFTTHAPPGDTLVHLDVSLFELFISGSIETILRDVVAAIL 651
Oy 612 GKGVGDVDFEKEATLASCANVRAITFYCDHVIKRDALOKVLEPTYSFHSFNILIT 671
Db 652 GKNDIFGEPVSLHOPKGSADVRAIITYCDLHQRADLLEVLMYPAFAESFMSKLEVT 711
Oy 672 YNLR 675
Db 712 FNLR 715

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DR InterPro: IPR002025; -
DR Pfam: PF000027; CNMP_binding; 1.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00914; CNG_membrane; 1.
DR PROSITE: PS00042; CNMP_BINDING_3; 1.
DR SMART: SM00100; CNMP; 1.
DR Ionic channel.
KW SEQUENCE 1102 AA; 123230 MW; A135CC36E2E7F1A3 CRC64;

Query Match 29.0%; Score 1452; DB 11; Length 1102;
Best Local Similarity 34.5%; Pred. No. 3.6e-100;
Matches 341; Conservative 201; Mismatches 340; Indels 106; Gaps 28;

Oy 8 RGLVAPONFELNINRSDNT--NPLYGNAQIY-DMPYIYSDNGPCKLSGYHRAEYMOKS 64
Db 5 KGLAPONTFLDTIATRFQGTSHNPLANAQAKGPPIYCSGFCGLGFAFTEYMOKS 64
Oy 65 STCSFMYGELTDKDTLEKRYQTFENYEMNSFELIMYKKNRTVPWFVKIAPIRNEODKYV 124
Db 65 CSCKFLFVETNMQMLQLEKSLSEKVEFEKGEIMFYKKNAGPFWCLLDIVPIKNEKGDYV 124
Oy 125 LFLCTFSDITAFKOP1-----EDSCKGWGR-ARLTRALTSRGVLOQLAPSVQKGENV 178
Db 125 LFLASFKDITDTKVKITSEDKKEDRAKGRSAGSHFDSARRSRALVYHISGHLQRRK- 183
Oy 179 HKHSLAEVLOLGSQI-----LPQKQKAPKTPPHIILHCYCFKFTWMDIILTFYTA 232
Db 184 -----NKLKINNNEFVDKPAPEYKSDAKSKFEILHFSFKAGMWMLILATFYVA 236
Oy 233 ILVPAVNSF-----KTQONNVAMLVDSIYDVILVILNFTTFVPAGEVISDPK 285
Db 237 VVPYVNCVIGMEDLSTSTYS----DIAVEILFIIDIIINFTTYKSGQVYFEAR 292
Oy 286 LIRMYLKTWEVIDLISCLPYVINAENFVNDGSISSLSKLVRLRLGVARAKLDHYI 345
Db 293 SICIHVVTFTIIDIALPDLVAF-NVT--VVSIVHLIKTVRLRLRLQKDRYS 349
Oy 346 EYGAVALVLCVFGLAHMACTIYSGDYELFEDDTITR-NSNMLYOLAMDIGTPQ 404
Db 350 OHSTIVLTLLSMFALLAMMACIYVIGKME--REDNSLWKEWGMHELKRLSESPY 407
Oy 405 FNGSGSGKWEKGSNSVYISLFTMTSLTSVGFGNIAFSTDEKIPAVAIMIGSLY 464
Db 408 GNNT-----LGGPSIRSATIATLFTLSSLTSGVGNVANSANTDAEITFICMILGALMH 462
Oy 465 ATIFGNVTTFIQQMYANTNRHYHEMLNSVRDLKLYQVPGKLSERVMDYIVSTWSKRGID 524
Db 463 ALVFGNVTATIIQRMYSRMSLYHTFRKDKDFIRVHHLPOQLQRMLEVFQYTWSVNNGID 522
Oy 525 TEKVLQICPKDMRADICVHLNRKVEKEHAPFRLASDGLRALAMEFYVHCAFGDLIYHA 584
Db 523 SNELKDEPDELRSIDITMHLNKEIL-QLSLFECASGKCRSLSLHKTISFCFAGEVILLQ 581
Oy 585 GESVDSLFPVYSGSELEVODDEVAAILGKGVGFQVFWKEATLASCANVRAITFYCDLHV 644
Db 582 GDALDAITFYVCSGMEVLDNSVLAHLGKGDILGANLSTKIDQYITKNADVLAITTCDDLOC 641
Oy 645 IKRDALOKVLEFYTAFSHSFNRN--ILTYNLKRKRIVKFIIDVYKREERKRRKNEAPL 702
Db 642 IILKLFLEVIGLYPEYAHKFVEDIQHDLTYNLR-----CHESDY-----ISRLSNKSTVQ 693
Oy 703 ILPPDH-PVRLRLOFRFOOKEARLAERGGRLDLDVEKGNVLTETHASANSLVKASVY 761
Db 694 AEPKNGSIKKRLPISVEDEEEVEEETTSLSP-----IYRGSVSHSKTKGS-- 744
Oy 762 TVRESPAPVPSQAASTSGVPHAKLOAPGSECLPCKGGGCGACARAKSKARKKDCGKSE 821
Db 745 ---SKSYLGLSLKQLTSGVPHSPIRV--SSANSPPK-----TKQEADPPN 785
Oy 822 DMNKVSKAESMETLPERTKASGEATLKKTDSCDSGITSLDLNVG-EARSPODR-SPI 879
Db 786 HGTREKMLKVOYOLCSLGTAGTPELSPRIYDGIEDNSSEETQTFDFGSGQIRPEPRISPS 845

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OY 860 LAEVHSHSPYIPEDOTLQATVLEVR-HELEKEDIKALNAKMTNIEKOLSE-----ILRLIL 931
DB 846 LG-----ESEIGAFAFLFIKAETFOQINKLNSEVTLTQEVSOIGKDMRSIMOLL 895
OY 932 TSSRSSQSPQELFEISRQSPSESDIF 959
DB 896 ENILSPQOPSPQCSL-HPTISICPSRESF 922

RESULT 15
O9ER47 PRELIMINARY: PRT: 1195 AA.
AC O9ER47;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ERG3 PROTEIN.
GN ERG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Arcangel A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ291608; CAC14797.1; -.
SO SEQUENCE 1195 AA; 135026 MW; 8DCB9BA0580FFC2 CRC64;

Query Match 28.7%; Score 1435.5; DB 11; Length 1195;
Best Local Similarity 30.4%; Pred. No. 7.1e-99;
Matches 368; Conservative 179; Mismatches 311; Indels 353; Gaps 31;

OY 7 RRGVLAPONTFLENTIVRSNDTN--FVLGNAQIVDPYVNSDGFCKLSGYHRAEYMKRS 64
DB 4 RGHVAPQPFELGTITIRKEGONKKFIANAVONCAIITCNDGJCEMGSFSPDYMKRP 63
OY 65 STCSMYGELIDKDTIEKYROTFFENTENMSFELMKKKRTPVFEVKIAPIRNEODKYV 124
DB 64 CTCDLHGPEYKRDHIAQIAQALLGSEERKVEVYTHKNGSTFICNTHTIIPVKNQGVAM 123
OY 125 LELCTFSDIT 134
DB 124 MFINFEYVTDENAAATPRVNPILPVKTVNKKLGFKFPGRLVLYTRKOSLPQEDPDVY 183
OY 135 -----AFKOP-----IEDDSC-----KG 147
DB 184 VIDSKSHSDSVAMKHKFPTKESCSPSADDTKALIQSOSPLVNIISGPLDHSPPKQ 243
OY 148 WGF-----ARLRALTSR-----GVLOQLAPSVOKGENV 178
DB 244 WDRLYPDMLOSSQLTHSRRESLCSIRASSVHDIIEGFSVHPKNIFRDRHASSEDNGRNV 303
OY 179 -----HKHS----- 182
DB 304 KGFPHIKSSLLGSTSDSNLNKRYSTINKIPQLTLNFSDVTEKKNTSPSSDKTIAPKV 363
OY 183 -----RLAEVLQIGSDILPOYKQEAAPKTPPHIILHYCVFKTWMQIILITFYTAI 233
DB 364 KERTINNVTEKYOVLSLGDVLPPEYKLOTPIRKFTIILHSPKAWMDLILLLVYTAI 423
OY 234 LVPYVNSF-----KTRONNVAML--VDSIVDVFILVDIVLNFHTTGVGPAGEVIS 282
DB 424 FPTYSAAFLLNDRERQKRECGYSCSPLNVVDLIDVIMFIIDILINFRTTYVNONEEVVS 483
OY 283 DPKLRMNLKTKWVFDLISCLPIYDYNFENVDEGISLFSKLVKRLRLGRVARKID 342
DB 484 DPAKIAIHFKWGMFLIDVAAIPFDLL-VFGSGSDETTLLIGLTKARLLRLVAVARKID 542

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OY 343 HYIENGAAVLVLLVCVGLAAHMACTWYSIGDY---IFDEDTKITIRNNSWLYQLAMD 399
DB 543 RYSEYGAAVLMLMCMIFALIAHIAHIACTWYIGVVERPYLTDK-----IGWLDISLGT 595
OY 400 GTPYQFNGSGSGWEGGPKNSVYISLVEPTMTSLTSGVGNLAPSTDEIKFAVAMMI 459
DB 596 GKRKYNDSSSS-----GPSIKDKYVATALYFTFSSLSVGVGNVSPNTSEKIFSLCVML 650
OY 460 GSLLYATIFGNVTTIPQMYANTNRYHEMLNSVRDLFLKLYQVKGSLSERMDYIVSTWSM 519
DB 651 GSLMTASIFGNVSAITQRLXSGTARHMQMLRYKEETIRFHQIYNPLRQRLSEEFQGANMTY 710
OY 520 SRGIDTEKYLQICPKDMRADICVHLNRKYKREHAPRLASDGLRALAMEFQVHCAPGD 579
DB 711 TNGIDNMNVILKGPPECLQADICLHNOTLLQNCARFAGANKGCLRALAMFKTHAPGD 770
OY 580 LYIHAGESVDSLCEVYSGSLVEYIODEVVAIILKGDFGVGFVKKEATLQASCANVALTY 639
DB 771 TLVHCGDVLTALYFLSRGSEIETLKDIIVAAIIGKNDIFGEMVHLAKPKGSNADVALTY 830
OY 640 CDLHVTKRDALQVLEFYTAFSHFSRNLITYNLRKRIYFRKISDYKREERMRKNE 699
DB 831 CDLHKIQREDDLEVLDMTPEFSDFLTNLLETNLHESA--KSQSYNDSGDTGK----- 884
OY 700 APLLPDPHPVRLFORFROQKEARLAERKGRDLDDVEKGNVLTENASANHSLVKAS 759
DB 885 -----LRRRLSPSESEGEKDFSKENSANDAD-----S 912
OY 760 VYTVRESPATPVSFQAASTSGVDPDHAKIAPGSECLGPKGGGDCAKRKSMARFKDACG 819
DB 913 TDTIRRYQSKKHFE-----ERKS--RSSSFIS 939
OY 820 SEDMNVKSAESMETLPERTKAS---GEATL-----KKTDSG--DSGITRSDLRLDN 866
DB 940 IDDEQKPLRGIVDSITPRMAYKATRLHGEETMPSPRIHTDKRSHSCDDITDTSWER--- 936
OY 867 VGEARS-PODRSPILAEVKHSFYPIPEOTLQATVLEVRHE--LKEDIKALNAKMTN--- 919
DB 997 -EPARAQPEECSP--SGIORAANGVSETESDLTYGEVGRQLDLQEQNLNLESQMTDIQ 1053
OY 920 -----TEKOLS-----ELRLIL-----TSKR---SSQSQDEL 943
DB 1054 AILQLOKQTTVPPAYSMVTAGAEOPLRLRLRTSHPRASIKTDRSFPSSQCPFD 1113
OY 944 FEISRQSPES 954
DB 1114 LEKSKLOSKES 1124

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Search completed: August 4, 2001, 11:38:49  
Job time: 148 sec

Sat Aug 4 14:48:50 2001

us-09-694-777-3.rspt

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GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: August 4, 2001, 11:34:56 ; Search time 24.05 Seconds  
(without alignments)  
2424.960 Million cell updates/sec

Title: US-09-694-777-3

Perfect score: 5001  
Sequence: 1 MTNAGRGRLVAPONTFLEN.....LFEISRPQSPESRDIFGAS 962

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq\_0601:\*

- 1: /SID58/gcgdata/geneSeq/geneSeq/AA1980.DAT:\*
- 2: /SID58/gcgdata/geneSeq/geneSeq/AA1981.DAT:\*
- 3: /SID58/gcgdata/geneSeq/geneSeq/AA1982.DAT:\*
- 4: /SID58/gcgdata/geneSeq/geneSeq/AA1983.DAT:\*
- 5: /SID58/gcgdata/geneSeq/geneSeq/AA1984.DAT:\*
- 6: /SID58/gcgdata/geneSeq/geneSeq/AA1985.DAT:\*
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- 8: /SID58/gcgdata/geneSeq/geneSeq/AA1987.DAT:\*
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- 11: /SID58/gcgdata/geneSeq/geneSeq/AA1990.DAT:\*
- 12: /SID58/gcgdata/geneSeq/geneSeq/AA1991.DAT:\*
- 13: /SID58/gcgdata/geneSeq/geneSeq/AA1992.DAT:\*
- 14: /SID58/gcgdata/geneSeq/geneSeq/AA1993.DAT:\*
- 15: /SID58/gcgdata/geneSeq/geneSeq/AA1994.DAT:\*
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- 18: /SID58/gcgdata/geneSeq/geneSeq/AA1997.DAT:\*
- 19: /SID58/gcgdata/geneSeq/geneSeq/AA1998.DAT:\*
- 20: /SID58/gcgdata/geneSeq/geneSeq/AA1999.DAT:\*
- 21: /SID58/gcgdata/geneSeq/geneSeq/AA2000.DAT:\*
- 22: /SID58/gcgdata/geneSeq/geneSeq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5001	100.0	962	AAV49944	Human potassium ion
2	4977.5	99.5	989	AAV49945	Human potassium ion
3	4844	96.9	962	AAV83032	Rat Eag1 potassium
4	3800.5	76.0	988	AAV31714	A human alpha-subu
5	1452	29.0	1102	AAV83028	Rat Elk1 potassium
6	1449.5	29.0	1107	AAV44907	Human potassium ch
7	1424	28.5	1163	AAV83031	Rat Erg1 potassium
8	1415	28.3	1159	AAV32020	Human cation chan
9	1415	28.3	1159	AAV85405	Long QT syndrome a
10	1414	28.3	1159	AAV85406	Long QT syndrome a
11	1370	27.4	1083	AAV44781	Human Elk voltage

12	1369	27.4	1017	20	AAV22427	Human brain specif
13	1369	27.4	1080	21	AAV77738	Human ESK1 (hESK1)
14	1369	27.4	1083	20	AAV22426	Human brain specif
15	1369	27.4	1083	21	AAV44904	Monkey potassium c
16	1369	27.4	1083	21	AAV44778	Human Elk voltage
17	1369	27.4	1083	21	AAV44779	Human Elk voltage
18	1369	27.4	1083	21	AAV44780	Human Elk voltage
19	1363	27.3	1083	21	AAV84835	Herq4, a potassium
20	1357.5	27.1	1082	20	AAV34128	Human potassium ch
21	1216.5	24.3	888	20	AAV17399	Human erg subfam1
22	1114.5	22.3	542	21	AAV44905	Human potassium ch
23	993.5	19.9	457	21	AAV77739	Human ESK1 (hESK1)
24	873.5	17.5	626	20	AAV17398	Human erg subfam1
25	747	14.9	145	21	AAV83115	Human secreted pro
26	747	14.9	145	21	AAV83117	Gene 40 human secr
27	734	14.7	145	21	AAV83116	Human secreted pro
28	734	14.7	145	21	AAV83118	Human secreted pro
29	687	13.7	141	21	AAV83030	Rat Eag2 potassium
30	512.5	10.2	910	20	AAV22191	Mouse brain CNG-1
31	502.5	10.0	755	20	AAV22192	Human brain CNG-1
32	486.5	9.7	774	21	AAV83115	Human hyperpolaris
33	478.5	9.6	767	20	AAV31227	Sea urchin Ih ion
34	472	9.4	598	20	AAV22194	Human brain CNG-2
35	468.5	9.4	528	20	AAV22193	Mouse brain CNG-2
36	465	9.3	506	20	AAV44906	Human potassium ch
37	439	8.8	506	20	AAV22195	Mouse brain CNG-3
38	386	7.7	824	20	AAV44001	A potassium channe
39	382.5	7.6	857	20	AAV32019	Arabidopsis thalia
40	376.5	7.5	662	20	AAV14585	A. thaliana potassi
41	367	7.3	707	21	AAV13545	Arabidopsis thalia
42	367	7.3	707	21	AAV52128	Arabidopsis thalia
43	367	7.3	733	21	AAV13544	Arabidopsis thalia
44	367	7.3	733	21	AAV52127	Arabidopsis thalia
45	362.5	7.2	873	21	AAV97876	Eucalyptus canald

#### ALIGNMENTS

RESULT 1.

ID AAV49944 standard; Protein: 962 AA.

AC AAV49944:

DF 31-JAN-2000 (first entry)

XX Human potassium ion eag channel protein #1.

DE Human potassium ion eag channel protein #1.

XX Human: potassium ion eag channel; K+ ion channel; cancer; gene therapy;

KW neurodegenerative disease; cell proliferation; diagnosis; tumour;

KW porlasis; neuroblastoma; cervix carcinoma; carcinoma;

KW breast adenocarcinoma; breast carcinoma ductal type;

KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;

KW lateral amyotrophic sclerosis.

XX Homo sapiens.

OS Homo sapiens.

XX MO9954463-A2.

XX PN MO9954463-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-EP02695.

XX PR 21-APR-1998; 98EP-0107268.

XX (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.

PA Parde-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;

PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;

DR WPI: 2000-013250/01.

DR N-PSDB; AA2357716.

XX New gene encoding human ion channel useful for diagnosis of, e.g.  
 PT cancer and neurodegenerative diseases -

PS Claim 1: Page 75-79; 89pp; English.

CC The present sequence is a protein (I) having a function of the human  
 CC K<sup>+</sup> (potassium) ion eeg channel. Analysis of the expression of the  
 CC polynucleotide encoding the protein (I) having a function of the human  
 CC K<sup>+</sup> (potassium) ion eeg channel (II) or quantitative presence of  
 CC (I) in cells of mammals such as human, rat or mouse is useful for  
 CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer  
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as  
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative  
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral  
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor  
 CC of the expression of (II) or an inhibitor or modifying agent of the  
 CC malfunction of (I) or (II) into a mammal disease caused by undesired  
 CC expression or overexpression of (II) or malfunction of (I) can be  
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also  
 CC useful for inhibiting cell proliferation. (II) can be used in gene  
 CC therapy for inhibiting cell proliferation or disease such as cancer or  
 CC psoriasis and is also useful for specifically detecting human eeg mRNA  
 CC in tissues, by employing the Northern blot technology. Diagnostic  
 CC compositions are useful in detecting the onset or progress of diseases  
 CC e.g. cancer related to the undesired expression or overexpression of (II)  
 CC and also for detecting malfunction of (I). They are further useful for  
 CC classification of tumours or the developmental status of tumour.

SO Sequence 962 AA:

Query Match 100.0%; Score 5001; DB 21; Length 962;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTYAGRGRLVAPONTLENIIVRSNDTNYLGNQIVDWPVYSNDGFCGLGYRAEV 60  
 DB 1 mtmagrrglvapntlfenivrrsndtnfvlgnadqldwplvysndgfcslgyhraev 60  
 OY 61 MOKSSTGSPWGEITDMDTIRKVRQTFENYEMNSFEILMYKKNRPVFPYKIAIRMD 120  
 DB 61 moksstsgspwgeitdmdtirkvrtfenyemnsfeilmykknrtprvfpkyaiarimdg 120  
 OY 121 DKVLLFTCFEDTIAFKOPIEDDSCKGKGFARLFRALTSSRGVLOQAPVQKENVHK 180  
 DB 121 dkvllftcfedtiafkopieddsckgkgrfartlratlssrgvlgqlapsvqkenvhkh 180  
 OY 181 HSRLAEVLQGLSDILPYKQEPKTPPHILHYCVFETTMWIIILTFYAILPVYNS 240  
 DB 181 hsrtaevlqgsdillpykqgeapktpphllhycvfcttwmiiilftfyailpvynvs 240  
 OY 241 FKTQNNVAVLVSYDVIFLVQIVLNFHTTFPGAGEVSDPKLIMNVIKTFVIDL 300  
 DB 241 fktqnnvavlvsydviflvqvivlnfhttfpgagevdsdpklimnvtiktfvidl 300  
 OY 241 fktqnnvavlvsydviflvqvivlnfhttfpgagevdsdpklimnvtiktfvidl 300  
 DB 241 fktqnnvavlvsydviflvqvivlnfhttfpgagevdsdpklimnvtiktfvidl 300  
 OY 301 LSCPLPYVIAFEFVNDGSSLSFSIKVYRLLRGRVARKLDHYTEYGAAYVLVCFVG 360  
 DB 301 lscplpyvinafefvndgsslsfsikvyrllrgrvarkldhyteygaayvllvcvfg 360  
 OY 361 LAAHMMACIWYSIGDYELFDEDTKTRNNMWLYOLAMDIGTPYQFNGSGSGKMEGSPKN 420  
 DB 361 laahmmaciwysigydyelfdedtktrnnmwlyqlamdigtpyqfngsgsgkwegspkn 420  
 OY 421 SVYISSLYFTMTSLTSGFGNIAPSTDEKIFAVAIMIGSLVATIFGNVTTIFQOMYA 480  
 DB 421 svyisslyftmtsltsgfgniapstdiekifavaimigsllyatifgnvttifqymya 480  
 OY 481 NTNRYHEMLNSVRFKIKYQVPGKISERVMDYISTWSMGSDIDEXVLIQCPKMRADI 540  
 DB 481 ntnryhemlnsvrfkikyqvpkgiservmidyistwsmgdidekvliqcpkmdradi 540  
 OY 541 CVHLNRKVFKEHPAFRLASDGLRALAMEFQTVHCAPGDLIYHAGESVDSLQFVVSGL 600

DB 541 cvhlmrkvfkehpafrlasdgclralamefqtvhcapgdllyhagesvdsldfvsvgl 600  
 OY 601 VTRODEVAAILGKGVFQGVFWKKEATLAOSCANVRALTYCDLHVIRDLQKYLEFYTA 660  
 DB 601 vtrodevaailkgvfvqgvfwkkeatlaoscanvraltycdlhvirkdlaqkylefytaf 660  
 OY 661 SHSFERNLLTYNLRKRRIYFRRKISDVKREEREMKRNKNEAPLLPDHPVRLFORROO 720  
 DB 661 shsfernlltynlrkrriyfrfrrkisdvkrreeremkrnkneapllppdhvrrlffrfrrg 720  
 OY 721 KCARLAEEGGDDLDLVKEKGNVLETHASANHSLYKASVYVYRESAPVPSQAASTSG 780  
 DB 721 kearlaaeggddldlvkekgnvlethasanhslvykasyvyvresapvpvsfqaastsg 780  
 OY 781 VVDHKLQAPGSECCIPKGGGGCAKRSWAPRKDCGKSEDMNKYSKASMETLPERFK 840  
 DB 781 vvdhklqapgseccipkggggcarkrswarprkdcgksedmnkyskasmetlperfk 840  
 OY 841 ASGEATLKKTDCSDGIRTSRLNDNVGEARSPQDRSPILAETHKSFYPIPEOTLQATVL 900  
 DB 841 asgeatlkktcdsgirtsrlndnvgearspqdrspilaethksfypipeqlqatvl 900  
 OY 901 EYRHELEKEDIKALNAKMTNIEKOLSEILRLTSRSGSQPELFEISRPOSPESENDIRG 960  
 DB 901 eyrhelekedikalnakmtniekolselrltssrsgsqpelfeisrpospeseridrg 960  
 OY 961 AS 962  
 DB 961 as 962

RESULT 2

AAV4945  
 ID AAV4945 standard; Protein: 989 AA.

AAV4945;

31-JAN-2000 (first entry)

DE Human potassium ion eeg channel protein #2.

XX Human; potassium ion eeg channel; K<sup>+</sup> ion channel; cancer; gene therapy;  
 KW neurodegenerative disease; cell proliferation; diagnosis; tumour;  
 KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;  
 KW breast adenocarcinoma; breast carcinoma ductal type;  
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;  
 KW lateral amyotrophic sclerosis.

OS Homo sapiens.

PN MO9954463-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99WO-EP02695.

PR 21-APR-1998; 98EP-0107268.

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;  
 Del Camino, Fernandez-Miranda D, Sanchez Perez A, Weseloh R;

DR WPI: 2000-013250/01.

DR N-PSDB: AA235717.

PT New gene encoding human ion channel useful for diagnosis of, e.g.

PS cancer and neurodegenerative diseases -

XX Claim 1: Page 79-82; 89pp; English.

XX The present sequence is a protein (I) having a function of the human



CC K+ (potassium) ion eag channel. Analysis of the expression of the  
 CC polynucleotide encoding the protein (I) having a function of the human  
 CC K+ (potassium) ion eag channel (II) or quantitative presence of  
 CC (I) in cells of mammals such as human, rat or mouse is useful for  
 CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer  
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as  
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative  
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral  
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor  
 CC of the expression of (II) or an inhibitor or modifying agent of the  
 CC malfunction of (I) or (II) into a mammal disease caused by undesired  
 CC expression or overexpression of (II) or malfunction of (I) can be  
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also  
 CC useful for inhibiting cell proliferation. (II) can be used in gene or  
 CC therapy for inhibiting cell proliferation or disease such as cancer or  
 CC psoriasis and is also useful for specifically detecting human eag mRNA  
 CC in tissues, by employing the Northern blot technology. Diagnostic  
 CC compositions are useful in detecting the onset or progress of diseases  
 CC e.g. cancer related to the undesired expression or overexpression of (II)  
 CC and also for detecting malfunction of (I). They are further useful for  
 CC classification of tumours or the developmental status of tumour.

XX Sequence 989 AA:

Query Match 99.5%; Score 4977.5; DB 21; Length 989;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 962; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 MTMAGRGRLVAPONTFLENIVRRSNDTFVLAQIVDWPDIYVNDGCKLSGYHRAEV 60  
 Db 1 mtnagrgrlvapontflenivrrsndtfvlgnaqivdwpdiysndgcklsghyhaev 60  
 QY 61 MQSSSTGCFMYGELTDKDTTEKVRQTFENEMNSFELIMKKNTPWFVKIPIRNEQ 120  
 Db 61 mqssstgcfmygeltdkdttekvrtqfemnsfelimkkntrpwfvlkkipirneq 120  
 QY 121 DKVYVLCFTGSDITAFKOPIEDSCGKMGKFAFLTRALTSRGVLAQOLAPSGKGENVHK 180  
 Db 121 dkvyvlfctgsditafkqpedscgkmgkfafltraltssrgvlgqlapsgvqgenvhk 180  
 QY 181 HSRRLAEVLQGSDLIPQYKQDAPKTPPHILHVCVFKTTDMWILLTFYVALLVPPYNS 240  
 Db 181 hsrllaevlqgsdliipqykqdeapktpphllhvcvfkttwdwlllftfyallvppyns 240  
 QY 241 FKTRQNNVAALVDSIVDFVLDIVNFTTFPGAGVGVSDPKLRMNTKWPVYDL 300  
 Db 241 fkttrqnnvawlvdsivdvlfvldivnfttfvpgagvgsdpklrmtwplkfwydl 300  
 QY 301 LSCLPDVINAFENVDE-----GISLFSLSLKVRRLLR 333  
 Db 301 lscldpvinafenvdevsafmgdpkqifadqipplpgressgslslslkvrrllr 360  
 QY 334 LGRVARKLDHYIEGAAVLVLCVFGIAAHMACIMYSIGDVEIFPEDTKTIRNNMWLY 393  
 Db 361 lgrvarkldhyieygaavllvllcvfglaahmaciwyssigdyelfdedektirnnswly 420  
 QY 394 QLAMDIGTPYQFNGSGSGKMGKSKNSVYISLFTMTSLTSVGFGLIAPSTDIKIFA 453  
 Db 421 qlamdigtpryqfngsgsgkmgksgksnsvyisslyfntsltsvfglriapstdekifa 480  
 QY 454 VAIMMGSLILYATIFGVWTTIFQOMVANTRYHEMLNSVRFLKLYQVPGLSRVDYXI 513  
 Db 481 valimmigslilyatifgvwtlifqymvantrryhemlnsvrflklygvpyglservdyxi 540  
 QY 514 VSTMWSRGIDTEKVLQICKDMRADICVHLNRKVFKEHPAFRLASGCLRALMEFQTV 573  
 Db 541 vstwmrsgidtekvlgicpckdmradicvhlntkrfkehpafriassgclralmefqtv 600  
 QY 574 HCAPGDLIVHAGESVSLCEVVSGLSEVIODEVAVALIGKGDVFGVFWKEATLAQSCAN 633  
 Db 601 hcapgdlivhagesvslcefvsglslevioedevavallgkgdvfgvfwkeatlaqscan 660

QY 634 VRALFYCDLHWIKDALQKLVLEFYTAFSHSFSRNLILTYNLKRRIVFRKISDVKREBER 693  
 Db 661 vralfycdlhwikrdalqkvlvlefytahsfnsfarnlllynlkrrivfrkisdvkreeer 720  
 QY 694 MKRRKEAPLILPPDHVPRRLPFRFRQOKEARLAERKGGDDDDLDVEKKNVLTERRSANH 753  
 Db 721 mkrrkeapllppdhvprrrlfrfrqokearlaeergddldlvekknvltetrsanh 780  
 QY 754 SLVKRSVTVRSPPTPVSFQASTSGVVDHAKLQAPGSECGPGGGGDCAKRKSWARF 813  
 Db 781 slvkrsvtvrspptpvsfqaastsgvvdhakiqapgsccgpgggdcakrkswarf 840  
 QY 814 KDACKSEDWKNVSKAESMETLPERTKASGEATLKRTDSCDGIKTSKDLNLQNVGEARSP 873  
 Db 841 kdacksedwknvskaesmetlpertkasgeatlkktdscdsgiktskdlrlnvgearsp 900  
 QY 874 QDRSTILAEVKHSFTRPFRQTLQATVLEVRHLEKEDIKALNKNINIEQISEILRILTS 933  
 Db 901 qdrstilaevkhsftrpfrqtlqatvlevrhlekedikalnkninieqiseilriltls 960  
 QY 934 RRSOSPOELFETSRPOSESESDIFGAS 962  
 Db 961 rrsospgelleistrpseserdifgas 989

RESULT 3

AA83032

ID AAY83032 standard; Protein: 962 AA.

AA83032:

04-JUL-2000 (first entry)

DE Rat Eag1 potassium channel membrane protein.  
 XX  
 XX ELK1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;  
 KW drug screening; hypertension; renal failure; diabetes insipidus;  
 KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;  
 KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;  
 KW sialorrhea; salivary insufficiency; membrane potential; current flow;  
 KW ion flux; transcription; signal transduction; assay; detection;  
 KW rat.  
 XX  
 XX Rattus rattus.  
 OS  
 XX  
 XX W0200012546-A1.  
 PN  
 XX  
 XX 09-MAR-2000.  
 PD  
 XX  
 XX 31-AUG-1999; 99WO-US19902.  
 PF  
 XX  
 XX 31-AUG-1998; 98US-0098413.  
 PR  
 XX  
 XX (UYNY -) UNIV NEW YORK STATE RES FOUND.  
 PA  
 XX  
 XX McKinnon D, Dixon JE;  
 PI  
 XX  
 XX WPI: 2000-256585/22.  
 DR  
 XX  
 XX Novel mammalian potassium channel genes and polypeptides encoded by  
 PT them for screening drugs useful for treating diseases such as  
 PT hypertension, acute renal failure, diabetes insipidus and  
 PT hypothyroidism -  
 PT  
 XX  
 XX Disclosure: Page 95-99; 102pp; English.  
 PS  
 XX potassium channel genes e.g. elk1, elk2 or eag2 are useful for  
 CC identifying modulators which are useful for treating hypertension,  
 CC acute and chronic renal failure, diabetes insipidus, diabetic  
 CC nephropathy, hypothyroidism, goiter, hyperparathyroidism,  
 CC pancreatic insufficiency, diabetes mellitus, cystic fibrosis,  
 CC sialorrhea, salivary insufficiency. The availability of the gene  
 CC sequences provides a tool for research into the physiological

CC characteristics of the various genes and proteins for potassium  
 CC channels including the development of medicines effective for  
 CC treating disease conditions associated with mutations or defects in  
 CC potassium channels and the screening of drugs to ensure that  
 CC potassium channels are not blocked or physiologically affected by  
 CC those drugs. The channel proteins encoded by these genes are also  
 CC useful themselves as reporter molecules in assay and detection  
 CC systems to measure changes in potassium concentration, membrane  
 CC potential, current flow, ion flux, transcription, signal  
 CC transduction, receptor-ligand interaction and second messenger  
 CC concentrations. See also GENESEQ records AA293334-293336.

XX Sequence 962 AA:

Query Match 96.9%; Score 484; DB 21; Length 962;

Best Local Similarity 97.0%; Pred. No. 0; Mismatches 16; Indels 2; Gaps 2;

Matches 934; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

QY 1 MTMAGRRGLVAPONTPLENIVRSNDTNEVLGNAQIVDWPIVSGNDGCKLGYHRAEV 60  
 DB 1 mtmagrrglvapontplenivrndtnfvlgnagivdwpivsgndgcklsgyhraev 60  
 QY 61 MOKSTGSGMIGELFDKTIKVKOTFENYEMNSEIIMYKKNRPWFVFIAPIRNQ 120  
 DB 61 moksstgsgmigelfdktkvkotfenyemnselilmykknrpwfvfiapirneq 120  
 QY 121 DKVVLFTFSDITAFKPIEDDSCGKMGKFAFLTRALTSNGVLOQLAPSVOKGNVVK 180  
 DB 121 dkvvlfctfsditafkpiieddscgkmgkfartlraltsngvlgqlapsvokgnvkh 180  
 QY 181 HSRLAEVLQSGDILPOYKQEAAPKTPHIIILHYCVK-TTMDIILILFTYALIVPVNV 239  
 DB 181 hsrlaevlqsgdilpykqeaap-pphllhyvfkttcwadlilftyalivpynv 239  
 QY 240 SEFTQNNVAMLYVDSIVDYVFLVIVLNFHTTTPGPGAGEVISEDKLIMNTLKTTFEVID 299  
 DB 240 sftqnnvamlvdsivdyvflvivilnfhttpgpagagevisedklimnylktvfid 299  
 QY 300 LLSCLPYDVINAFENVNDEGISLSFSLKVRLLRLGRVARKLDHYIEYGAVALLVCFE 359  
 DB 300 llsclypdivinafenvndegisslsfkvvrlrlgrvarkldhyieygaavalvvcvf 359  
 QY 360 GLAAHMACIWSIGDYEFEDETRTIRNNSWLYQLAMDIGTPYONGSGSGKWEGPSK 419  
 DB 360 glaahmaciwsigdyefedetktrnnswlyqladigtpyongsgskwegpsk 419  
 QY 420 NSVYISSLFTFTSLTSGFGNIASTDEKIFAVAIMIGSLVATIFGNVTTIFQGMK 479  
 DB 420 nsvyisslftftsltsgfgniastdekifavaimigslvatifgnvttifqgmy 479  
 QY 480 ANTNNYHEMLNSVRDLKYQVPGKLSERVMKYIVSTMSMSGIDPEKLIQICPKMRAD 539  
 DB 480 antnnymhlnsvrflklygvpkgservmkyivstmsmsgidckkylqicpkmrnd 539  
 QY 540 ICVHLNRKVFKEPAPRLASDCLRALAMEFQTVHCAPDLIYHAGESVSDLCFFVSGSL 599  
 DB 540 icvhlnrkfvkepafrlasdgclralamefqtvhcapdliyhagedsdscffvsgsl 599  
 QY 600 EYIODEVVAIIIGKDVFGDVFWKEATLAOSCANRALTYCDLHVIRKDALOKVLEFYTA 659  
 DB 600 eyigdeevaaiigkdvfgdvfwkeatlaoSCANRALTYCDLHVIRKDALOKVLEFYTA 659  
 QY 660 FSHSRNRNLIILYNNRKRIYERKISDVKEEFERMRKKEAPLILPPDPVRLRPRRFO 719  
 DB 660 fshsrnrnliilynnrrkriyerkisdvkefeermrkkeapilppdpvrrlprrrfo 719  
 QY 720 QKEARLAAERGRDLDLDERKGNVLTETHASANHSLYKASVTVRESPPATPVSFQAAST 779  
 DB 720 qkearlAAERGRDLDLDERKGNVLTETHASANHSLYKASVTVRESPPATPVSFQAAST 779  
 QY 780 GVPDHAKIQAPESECLGPGGGDCAKRKSMARFQDACKSGSEDMNFKVKAESMETLPER 839  
 DB 780 gvpdhakiQAPESECLGPGGGDCAKRKSMARFQDACKSGSEDMNFKVKAESMETLPER 839

DB 780 tvsdhaklhapseclgpkagggdpakirgyvarfkacgkgedwnvksaesmetlper 839  
 QY 840 KASGENTLKTSDSCGIRKSDRLDNVGEARSPDRIAEVKSFPYIPOTLOATV 899  
 DB 840 kasgentlktscdsgirksdrldnvgearspdrialevksfypipotlqatv 899  
 QY 900 LEVHELKEDIKALNAKMTNIEKOLSEILIRILTSRSSSPQELFISRPQSPESRDIF 959  
 DB 900 levhelkedikalnakmtsiekselilrilsrssspqelcivsrpqspsrdif 959  
 QY 960 GAS 962  
 DB 960 gas 962

RESULT 4

ID AAB31714 standard. Protein; 988 AA.

AC AAB31714;

DT 30-APR-2001 (first entry)

DE A human alpha-subunit of voltage-gated potassium channel (Eag2).

KW Alpha-subunit; voltage-gated potassium channel; Eag2; ion flux;

KW central nervous system disorder; migraine; hearing; vision; stroke;

KW Alzheimer's disease; memory disorder; seizure; psychotic disorder.

OS Homo sapiens.

PN WO200104133-A1.

PD 18-JAN-2001.

PF 12-JUL-2000; 2000WO-US18898.

PR 13-JUL-1999; 99US-0143467.

PA (ICAG-) ICAGEN INC.

PI Jegla TJ, Liu Y;

DR WPI; 2001-138308/14.

PT N-PSDB: AAF25271.

PT Novel alpha subunit of potassium channel for identifying modulators of

the channel for use in treating disorders involving abnormal ion flux,

e.g. central nervous system disorders -

Claim 21; Page 60-61; 75pp; English.

The present sequence represents an alpha-subunit of a voltage-gated

potassium channel. The polypeptide is designated Eag2. The polypeptide

is useful for screening activators or inhibitors of voltage-gated

potassium channels that contain an Eag2 subunit. Modulators of

voltage-gated channel activity are useful for treating disorders

involving abnormal ion flux, e.g. central nervous system (CNS)

disorders such as migraines, hearing and vision problems, Alzheimer's

disease, learning and memory disorders, seizures, psychotic disorders

and as neuroprotective agents e.g. to prevent stroke. Eag2 is useful

as a reporter molecule to measure changes in potassium concentration,

membrane potential, current flow, ion flux, transcription signal

transduction, receptor-ligand interactions, second messenger

concentration in vitro, in vivo and ex vivo, and also as indicator of

current flow in a particular direction. Detecting Eag2 nucleic acid

and protein expression is useful for diagnosing disease caused by

abnormal ion flux. Eag2 nucleotide and amino acid sequence information

may also be used to construct models of voltage-gated potassium channels

in a computer system.

Sequence 988 AA:

Query Match 76.0%; Score 3800.5; DB 22; Length 988;  
 Best Local Similarity 73.7%; Pred. No. 0;  
 Matches 735; Conservative 96; Mismatches 111; Indels 55; Gaps 12;

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QY 3 MAGGRGIVAPONTFLEIVIRSRNDTNVLAQAIVDMPYVYNDGFCLSGYHRAEYMO 62
  1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  1 mp9gkrlvqpnfflenivrrssesfllqnaqlvdpvysndgfciksgyhradwqm 60
  DB KSSNCSFYGLTJDKDTEKROPEENEMNSFEILMTKKNTPWPFKTAIPINEDDK 122
  63 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  61 ksscsfmygeltdkktlekrqtdmnescevllykknrtcpwfygmqlapirnehek 120
  QY 123 VLFELTFSDITTAFCOPLEDSDCKGKFAFLTRALTFSSRGVLAQOLAASVOKGENVHKS 182
  121 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  121 vlfelctkdtlftkqpredstskwtckfartlraltnsrslvglltp-maktevvhks 179
  QY 183 RLAEVLQGSILPOLYKOAEKTPPHILHYCVERKTWDMILITPYTALIVPVNSFK 242
  180 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  180 rlaevlqgsdlbpqkgeapktpphillhycafkltwvlllftfyalnvpyvnsfk 239
  QY 243 TRONNVAMLVDSIVDVLELDIVLNFHTFVGPAGEVISOPEKLRIMVTKRWFIIDLS 302
  240 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  240 tkqnlavlvdsivdvlfvdlvlnfhtlvpggevisdpkllrmylktwfvdlis 299
  QY 303 CLPYDVINAFENVEGISTLFSLSKVVRLRLGRVARKLDHYIEYGAVALVLCVFGIA 362
  300 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  300 clpydlnafenvdegisslfsislkvrrllrlgrvarkldhyleygaavvlvlvcfglv 359
  DB 363 AHMACIWSIGDYEIEDEDTKTIRNNSWLYOLANDIGTPYOFNGSGSGKMGSPKNSV 422
  360 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  360 ahwlaclwyslgdyevldentlqidswlyqlalslgtpryntcs-agiwegpskds 418
  QY 423 YISSLYEFTMSLTGVTGNTAPSDIEKIFAVATIMIGSLIATFEGVNTTFQOMVANT 482
  419 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  419 yvsslyftmstlctlgtnlaptcdvckmfsavmmvsglllyatlfgvntlftqmyant 478
  DB 483 NRYEEMNSVDFPLKLYOPKGLSERVNDYIVSTWSMGRGIDTEKVLQICPKDMADICV 542
  479 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  479 nryhemlnvrdflklygvprglservndyivstwsmskgldtekvlsicpkdmradicv 538
  QY 543 HLNKRVKEHPARPLASDGLRALAMEFQVHCAPAGDLIYNAGESVDSLCEYVSGSEVI 602
  539 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  539 hlnkrvkehpaprplasdglralamefqtvcapagdllyhageevdalcfcvsgslev 598
  QY 603 ODDDEVAILGKGDVFGDVFWEKATLAOSCAVNRATYCDLHVIRKDALQKVIETASH 662
  599 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  599 qddevaillgkgydvfgdflwketlhaacavnraltycdlhlikrealikvldiyatan 658
  DB 663 SFSNRLITTYMLRRRIYFRKISDYKREEEEMKRNENAPLILPRHPVRLFORROOKE 722
  659 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  659 sfsnrlitcnlrrlfrklsdykkeeelrqknevtlspvdpvprkflfgkikqke 718
  QY 723 ARLAERGRDLDLVEKGNVLTETHASANN-SLVKASVYTVRSPATPVSFQAASVSG 780
  719 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  719 lngsgtsgv-----dpegnlqyestsrlngtstlgsavtl-sqtlpq-----tslay 767
  DB 781 VPDIAKLAQESSECLGPKGGG---DCAK-----RKSWAREFDACG---KSED 822
  768 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  768 vktseaslqgnrdamelkpnagadqclkvnsplrmknngkywrlrknmgahkeeked 827
  QY 823 MNKYSKASMETLPERKASGEAT-----LAKNDSCSGITKSDRLDNGGEARSPDR 876
  828 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  828 mnyvltkaesmgllsedpkssdsensvtnkprltdscsgltdskldkageaaspleh 887
  QY 877 SPILAEVKHSFYPIPEDTLQATVLEVRHELKEDIKALNAKNTNEKQSLERILITL 932
  888 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  888 spilaedkhnpyrpedagqlcttlqevkhekedqllscrtalalekqvaelikltskxv 947
  DB 933 ---SRSSQSP-----DELFEISRPOSPEBERD 957
  948 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  948 pqasprksqmplgyvppqlpcqdlfsvsrpspsedkd 984
  
```

```

RESULT 5
AAV83028
ID AAV83028 standard; Protein; 1102 AA.
XX
AC AAV83028;
XX
DT 04-JUL-2000 (first entry)
XX
DE Rat Elk1 potassium channel protein.
XX
KW Elk1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;
KW drug screening; hypertension; renal failure; diabetes insipidus;
KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;
KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;
KW sialorrhea; salivary insufficiency; membrane potential; current flow;
KW ion flux; transcription; signal transduction; assay; detection;
KW rat.
XX
OS Rattus rattus.
XX
PN WO200012546-A1.
XX
PD 09-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US19902.
XX
PR 31-AUG-1998; 98US-0098413.
XX
PA (UANY ) UNITV NEW YORK STATE RES FOUND.
XX
PI McKinnon D, Dixon JE;
XX
DR MPI: 2000-256585/22.
XX
DR N-ESDB: AA293334.
XX
PT Novel mammalian potassium channel genes and polypeptides encoded by
PT them for screening drugs useful for treating diseases such as
PT hypertension, acute renal failure, diabetes insipidus and
PT hypothyroidism -
XX
XX
PS Claim 29; Page 82-86; 102pp; English.
XX
CC Potassium channel genes e.g., elk1, elk2 or eag2 are useful for
CC identifying modulators which are useful for treating hypertension,
CC acute and chronic renal failure, diabetes insipidus, diabetic
CC nephropathy, hyperthyroidism, goiter, hyperparathyroidism,
CC pancreatic insufficiency, diabetes mellitus, cystic fibrosis,
CC sialorrhea, salivary insufficiency. The availability of the gene
CC sequences provides a tool for research into the physiological
CC characteristics of the various genes and proteins for potassium
CC channels including the development of medicines effective for
CC treating disease conditions associated with mutations or defects in
CC potassium channels and the screening of drugs to ensure that
CC those drugs. The channel proteins encoded by these genes are also
CC useful themselves as reporter molecules in assay and detection
CC systems to measure changes in potassium concentration, membrane
CC transduction, receptor-ligand interaction and second messenger
CC concentrations.
XX
XX
SO Sequence 1102 AA;

```

Query Match 29.0%; Score 1452; DB 21; Length 1102;  
 Best Local Similarity 34.5%; Pred. No. 19e-125;  
 Matches 341; Conservative 201; Mismatches 340; Indels 106; Gaps 28;

```

QY 8 RGLVAPONTFLEIVIRSRNDT--NFVLGNAQIV-DMPYVYNDGFCLSGYHRAEYMOKS 64
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  5 kglvapontfletiatrtfgtthsnflanaqyvakgfpryvcsgdfcfeiaqfatetvmqks 64
  DB
  
```

OY	65	STCSFMGELTDKDTIEKVROTFFENTENSEFELIMTKKNPTPWFEVFKIAPINEDOKV	124
Dd	65	cskfiflfgveineqimldjeiksleekvefknglmfykkngapfwcllldivipknekxv	124
OY	125	LFLCFHSQITAFKQPI-----EDDSCGMNGKF-ARLIRALTSSNGVLQOLAPSVOGENV	178
Dd	125	llfslafklctkvltksiedckkedragrsnagshfsdsarrtsnavlyhshqlqrck-	103
OY	179	HKHSRLAEVLIGSDI-----LRQYKOEAKPRTPHILHNCVEKTMWDNIIILPEFYTA	232
Dd	184	-----nkikinnvfcdkpafrpykvsdkkskfillhfstlkagwdwlllatflyva	236
OY	233	ILVPYNVSF-----KTRQNNAVLVDSDIVDFLVLDVLEHTTFVGPAGEVISDPK	285
Dd	237	vtyrvpvcflignedtstrrtsts----dlaveillfdilinftryevaksgvyfear	292
OY	286	LIRNMVLTWNVVIDLSCLPRDYVNARENNDEGISLFSSIKVVRLLRGRVARKLHDYT	345
Dd	293	siclhlyvtwtwidlaaipdfdllyaf-nvt-vvsvlvhlktvrlilrllqklidrys	349
OY	346	EYGAVLVLLVCVFGLAAMMACIMWSIGDIETDEPFTKR--NSWLYLOLADIGPYO	404
Dd	350	qbstvlvcllmsfmflahmacilyyigkne--rednsllkwevgylhegkrlespyy	407
OY	405	FNGSGSGWEGSPSKNSVYSISLYFTMTSLTSVGFGNIAPSTDIEKIFAVAIMMIGSLY	464
Dd	408	gnnt-----lggrsirsayiaalyftlsislsvgfigvnantsdaekffistcmllgblmh	462
OY	465	ATIPFNNTTIOQMAYANRNKHENHINSRDRLKIXOPKGISEVMVIYSTMSMGID	524
Dd	463	alvfgnvtaiqmrysrwslyhtctkdldlfirhlpqklkgmqleyfgtlcswvngid	522
OY	525	TEKVNLCPKMDRADICHLNRKKFKKEHPARLASDCGLRALNAEPOTVCAPDLTYHA	584
Dd	523	snellkdpdrstsdtmhnlkeil-qstlfecasrgclsishiktscapgeyllrq	581
OY	585	GESVDSLCEVVSGSLEVLIQDBEVALLGKGDVFDGVFWKEATTLAQSCANRYCDLHV	644
Dd	582	gdalgaifyfcvsgamevulkdmvtaillgqgliganlsikdgvlknadvakaltyclgc	641
OY	645	IKRDLQKLVLEYTTAFHSFSFRNL--ILTYYLKRIYFRKISDYKREEBRMKKNAPL	702
Dd	642	lllklglevlglypeyahkivediqhdltlyhre---ghesdv---lsrlnskstvq	693
OY	703	ILPPDH-PVRRLFOFRFOOROEARKLAERAGRGDRDLDDVEKGNVLTENASNHSLVKRASV	761
Dd	694	aepkngsrikrlpsiveeeeeeeetslsp-----lytrssvshsktys--	744
OY	762	TWRSPATPVSFQAAGSTGCVPDHAKIAQAPGECGLPKGGGDAKRRSMARFKDACGSE	821
Dd	745	-----sksyglislikqltsgtgyprhsplr-v-sanspk-----tkgeadpn	785
OY	822	DMNKYSKAESMTLPERRKASGEATLKTTDSGITYKSJDLRLDNV-EARSPODR-SPI	879
Dd	786	hgtrtekmlkyalslagrpelspirvdgidedgnseeetqtldfigeqrlpepirsps	845
OY	880	LAENVKSHFPDEQQLQATVLEVR-HEIKEDIKALNAKTMIKOLSE-----ILRIL	933
Dd	846	lg-----eseigaaffikeekkgqnlksevtlltqvavqlygkdmrsmingll	895
OY	932	TSRRSSQPDELFEISRQSPESERDIF	959
Dd	896	enllspqpsqfcsi-hptslspresf	922
RESULT	6		
AAY44907			
ID	AAY44907	standard; Protein; I107 AA.	
XX	AAY44907:		
XX			
DT	18-May-2000	(first entry)	

DE	Human	potassium channel molecule ERG-LP2 full-length protein.	
XX	Human;	potassium channel molecule; ERG-like protein 2; ERG-LP2;	
KW	neuroprotective;	antiparkinsonian; anticonvulsant; antidepressant;	
KW	neuroleptic;	nootropic; treatment; CNS disorder; central nervous system	
KW	potassium channel mediated disorder;	epilepsy; Alzheimer's disease;	
KW	Parkinson's;	multiple sclerosis; depression; schizophrenia; amnesia;	
KW	chromosome 3p21.3-24.3.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
EH	Domain	295..335	
ET		/note= "Transmembrane region cyclic nucleotide gated channel domain"	
ET	Modified-site	320	
ET		/note= "N-glycosylated"	
ET	Modified-site	409	
ET		/note= "N-glycosylated"	
ET	Modified-site	439	
ET		/note= "N-glycosylated"	
ET	Modified-site	468	
ET		/note= "N-glycosylated"	
ET	Modified-site	617	
ET		/note= "N-glycosylated"	
ET	Modified-site	687	
ET		/note= "N-glycosylated"	
ET	Modified-site	821	
ET		/note= "N-glycosylated"	
ET	Modified-site	953	
ET		/note= "N-glycosylated"	
ET	Modified-site	63..65	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	126..128	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	159..161	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	216..218	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	250..252	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	329..331	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	413..415	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	616..618	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	683..685	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	733..735	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	741..743	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	749..751	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	771..773	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	807..809	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	830..832	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	1078..1080	
ET		/note= "Protein kinase C phosphorylation site"	
ET	Modified-site	10..13	
ET		/note= "Casein kinase II phosphorylation site"	
ET	Modified-site	17..20	
ET		/note= "Casein kinase II phosphorylation site"	
ET	Modified-site	83..86	
ET		/note= "Casein kinase II phosphorylation site"	
ET	Modified-site	126..129	
ET		/note= "Casein kinase II phosphorylation site"	
ET	Modified-site	138..141	
ET		/note= "Casein kinase II phosphorylation site"	

Query Match	Score	DB	Length
Best Local Similarity	33.68;	Pred. NO. 3.4e-125;	
Query Match	29.08;	Score 1449.5;	DB 21; Length 1107;
Best Local Similarity	33.68;	Pred. NO. 3.4e-125;	

	Matches	337:	Conservative	198:	Mismatches	296:	Indels	171:	Gaps	27:
QY	8	RGVLAPQNFLEINVRNSMT--	--NFVLGNAQIV-DMPVIYSNDGFCUKSGYHRAEWMOKS	64						
Db	5	kglapqnfllatrlatrfdgthsnflanaayakgfpivcsdgfcjclagfartewmqs	64							
QY	65	SNCSFMYGGLTQDKDTIEKQRTQFENTENMSFELIMTKKRTTPVFWFVVIAPIRNODQWV	124							
Db	65	csckllfyetueqjmlqleaksleeketfxgelmtykknspfwclldvplknekadv	124							
QY	125	LLLCFSDITTAARQKPI----	EDDSCKGKGF--ARLTRLATSSRCVLOOLAPSVOKGVN	178						
Db	125	llfllskdldtckvkrltpeckkedkvgrstrgthfndssrrrrstrvllhysghlqtrek-	183							
QY	179	HKHSRLAEVLAQSGDI----	LPQYKQEARPTPHILHVCFTWDMWILLTFEYTA	232						
Db	184	-----nkikinnvfvdkpafpeykvsdaksrkflllfstfcagwdwlllllatfyva	236							
QY	233	ILVPTVNSF-----	KTRQNNVAHLVYDSIYDVLFVLDIVYNFTTTPYVGRAGEVISDPK	285						
Db	237	vevpyvncflgnddststrstvs---	dlaveillfllidllhltfitysksgyvlfaar	292						
QY	286	LIRMNVLKFWFIYDILDLSCRPDYVNAFENVDGSISSFLSKLVNRLIRGRARLADHYI	345							
Db	293	sclihyvtctwflldlaaapfdllayaf-nvt--vsvlhlklvtvlllllltllqldldys	349							
QY	346	EXGAANVLLVLCVFGLAHMMACIWSYISGDYEFEDBRTKIR--NNSWLYOLAMDIGTPYQ	404							
Db	350	qststlfltlmsfallahmaciwyvlgkme--	redonllkwevgvllhelgkrlsipy	407						
QY	405	FNGSGSGKKEGGPRKSNVYISSLFTYTMISLTSVSGGNLAPSPDIEKIRAVAIMIGSLLY	464							
Db	408	gnnt-----lpgpslrtsaylaalytlstlsavgfgvnsantdaekllstclmllgalmh	462							
QY	465	ATIFGNTVTFPOOMANTRTYHEMNSVDFKLLOVQPGLSERMDYVTSWSSKRGD	524							
Db	463	alvfgnvtaifgrmryselyhtrtkdkldkdfirvhhlpqllqgmrlqfyfctwsvngid	522							
QY	523	snellkdfpdelstrsdltmhlnekl-qslsfecarsgcltrslshlksfcapgeyllrq	581							
Db	585	GESVSLCPVSGSLLEVIODDEYVALILGKGVFGDVFWEKATLQASCANVRLITCDLHV	644							
Db	582	gdalqalyfvcsgsmevlkdsmviallbgldlganlsldqvlktnadvkaltcydclqc	641							
QY	645	IKRDALQKLEFYTAFSHSFNRLL--ILTYNLRK-----	RI-----	678						
Db	642	lllklalfeyldipyeyahkfyedighdltlmyrtreghescdvlsrlnkskmvsgepknng	701							
QY	679	VERKISDVKREEREEERMKRKNENAPLILPPDHVPYRLRFQFRQOKEARLAEARGRDLDLD	738							
Db	702	lnkrlpslveeaeaeaeaealsp-----lctgssrnkkvsgnksaylglskq	755							
QY	739	VEKGNVLTEHNASNLSLKASVYIVRESAPVPVSOAASITSGVDHAK-----	786							
Db	756	lasgfv-----pflspplr-----vrsnsapklqgldp-----	phnkrkexnlkqlst	800						
QY	787	LQAPSECIQPGKGGGDCAKRKSMARFPDADCKSDHMKVSKAESMELLPEPTKASGEAT	846							
Db	801	lnnaaprpalsrlivg-----	lactgnssesqldfygse-----	835						
QY	847	LKKTSCDSGITKSDLRLDNWGEARSPODRSPFLLAEVNHSEFYPIEQTLQATVLEVR--	HE	905						
Db	836	-----ltssepriap-----	plgdpdelgaavllikkee	862						
QY	906	LKEDIKALNAKNTNIEKQLSF-----	ILRLTISRSSQSP	940						
Db	863	tkqginklinsevtlltgevsgjkgcmrnvirllenvlspqgp	904							

RESULT 7  
AAV83031

ID AAY83031 standard; Protein: 1163 AA.  
 XX  
 AC AAY83031;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Rat Eragl potassium channel membrane protein.  
 XX  
 KW ELK1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;  
 KW drug screening; hypertension; renal failure; diabetes insipidus;  
 KW diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;  
 KW pancreatic insufficiency; diabetes mellitus; cystic fibrosis;  
 KW salivary gland; salivary insufficiency; membrane potential; current flow;  
 KW ion flux; transcription; signal transduction; assay; detection;  
 KW rht.  
 XX  
 OS Rattus rattus.  
 XX  
 PN W0200012546-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PE 31-AUG-1999; 99WO-US19902.  
 XX  
 PR 31-AUG-1998; 98US-0098413.  
 XX  
 PA (UYN) UNIV NEW YORK STATE RES FOUND.  
 XX  
 PI McKinnon D, Dixon JE;  
 XX  
 DR WPI: 2000-256585/22.  
 XX  
 PT Novel mammalian potassium channel genes and polypeptides encoded by  
 PT them for screening drugs useful for treating diseases such as  
 PT hypertension, acute renal failure, diabetes insipidus and  
 PT hypothyroidism -  
 XX  
 PS Disclosure: Page 90-95; 102pp; English.  
 XX  
 CC Potassium channel genes e.g. elk1, elk2 or eag2 are useful for  
 CC identifying modulators which are useful for treating hypertension,  
 CC acute and chronic renal failure, diabetes insipidus, diabetic  
 CC nephropathy, hyperthyroidism, goiter, hyperparathyroidism,  
 CC pancreatic insufficiency, diabetes mellitus, cystic fibrosis,  
 CC sialorrhea, salivary insufficiency. The availability of the gene  
 CC sequences provides a tool for research into the physiological  
 CC characteristics of the various genes and proteins for potassium  
 CC channels including the development of medicines effective for  
 CC treating disease conditions associated with mutations or defects in  
 CC potassium channels and the screening of drugs to ensure that  
 CC potassium channels are not blocked or physiologically affected by  
 CC those drugs. The channel proteins encoded by these genes are also  
 CC useful themselves as reporter molecules in assay and detection  
 CC systems to measure changes in potassium concentration, membrane  
 CC potential, current flow, ion flux, transcription, signal  
 CC transduction, receptor-ligand interaction and second messenger  
 CC concentrations. See also GENESDB records AA293334-293336.  
 CC  
 XX  
 SO Sequence 1163 AA;  
 XX  
 Query Match 28.5%; Score 1424; DB 21; Length 1163;  
 Best Local Similarity 30.4%; Pred. No. 8.5e-123;  
 Matches 362; Conservative 167; Mismatches 307; Indels 356; Gaps 32;  
 XX  
 QY 7 RRGVAPONTFLENTIVRR--SNDTFNVLGNAQIVDMPIVYSNDGFCGLSGYHRAEYMQRS 64  
 DB 4 RRGVAPONTFLENTIVRR--SNDTFNVLGNAQIVDMPIVYSNDGFCGLSGYHRAEYMQRS 64  
 QY 65 STCSMGELGELDKDTEKVKRTPFENTEMSFELMTKKRTPVWPFVKAPLRNEDDKYV 124  
 DB 64 ctcdlghprrtrraaaqaaqlgaeeerkvelafyrkdgscflclvdvvpvknedgavi 123

QY 125 LFLCTFS-----DITAFKPIE-- 141  
 DB 124 mfilnfewmekdmvsgpahdnhrpgrstslasgraktfrklpallalatarespmrtg 183  
 QY 142 -----DDSGCKGCKFARLRAL----- 158  
 DB 184 stgspgavavvdvdltpaapseslaldesamdnhvaglgp-aeerrtalvpgasasp 242  
 QY 159 -----TSSR----- 162  
 DB 243 vasiqphpspragslnpasgssclarttrrescasvrrassaddieamragalprrp 302  
 QY 163 -----GVLRQ-----DA 169  
 DB 303 rhasigamhplrsqllnstsdsdlvryrtlsktpqltnfnvdlkgpflaspsdrtella 362  
 QY 170 PSYQKGENVHK-HSRLAELVLAGSDILPOYKQEAPEKTPPHILHKEVFTDMITLIT 228  
 DB 363 ptk-erthvtekvtylsigadvlpeykqaprlhrtwllhyapfkxavdwlllliv 420  
 QY 229 FYTALVFNVSF---KTRQNNVA-----WLVVDSIVDVFILVDVILNFHTFVG 276  
 DB 421 lrtavtlypsaaflketedsqapdcyagcpplavvdlvdimfivdlinftrtyyna 480  
 QY 277 AGEVISDPKLIRNNYLTKEFWVIDLSCLPYDVYNAPENDEGISLSSLKVVRLRLGR 336  
 DB 481 neevshprlavhvfykgyflldmvaalpfdll---ifgsgeelilgllkarllrlvr 536  
 QY 337 VARKLDHTEKGAVALVLCVFGGLAAHMACIWSIGYEIRDEPTKTRNNSLYOLA 396  
 DB 537 varklidryseyaavllfmlctfallahwlaclwyaigmeqphms---hgwihng 592  
 QY 397 MDGTFYQFNGSGKWEKSGKNSYISLTYTMTSLTSGVGNIAPTSDIKIFAVAI 456  
 DB 593 dqtgkpy--nsqgl---gppsikdkyvalyftfslsvsgfmgspnteskisicv 646  
 QY 457 NMIGSLVATIFGQNTTIFQOYANTNRYHEMLNSVRDELKLYQVPGKLSERVADYIVST 516  
 DB 647 mlgsilmyasifgnvsaaligrlysgtaryhltqmlrvrefirfqjpnrlrleeyfqa 706  
 QY 517 WMSRSQIDTEKVLQITCPKMDRADICVHLNRKVKKEPARPLASDGLRALAMEFOVHCA 576  
 DB 707 wstytngidmnavlkqfpeclqadclhlnrslqhkpfqakgcylralamfkthp 766  
 QY 577 PGGLYHAGSVSYLGFVYSGSLEVIODDEVAIILKGDFGVFEMKEATLAOSCNVRA 636  
 DB 767 pgdliyahagdlialyflsrgseililrgdvvaalghndifgeplnlyarpyksngdvt 826  
 QY 637 LTYCDLHVLRKDALQVLEFYTAFSHSFNRLLITLYNLRRKRIYFRKISDYKREERMR 696  
 DB 827 ltycdlkhkhrddlllevldmrypfsdhfwesleifnlr-----dtn----- 868  
 QY 697 KNPAPLILPDDHVRVRLFORFOQKEARLAERGRDLDDLVYKGNVLTETHSANHSILV 756  
 DB 869 -----mlppspasaelsgfnrqkrklisfr-----rtldkdeg----- 903  
 QY 757 KASVTVRESPPARPVFQQAASGVDPDHAKLQAPGSECLGPKGGGCAKRSQWAFKDA 816  
 DB 904 pgevsaalqgpar-----vgpqsctgpgp-----pw----- 931  
 QY 817 CGKSEDMNKVSKAESMETLIPERTKA-----SGEATL-----KRTDSCD- 854  
 DB 932 -gespspspspspspsdepgyrspprlrlvpfsspppdsppggrpltdedgksdncp 990  
 QY 855 -----SGITKSDLRLDNV-----GEANSPO-----DRSPILAEVKAHSFYPIPEQTLQATVLE 901  
 DB 991 lsgafsgvs-----nifsgdsgrygqelprcpapap---sltnhp---laspgr 1037  
 QY 902 VRHELEKEDIKALAKMTNTEKOLS-----ELRLITSRRSSQSPQELFEISR 949  
 DB 1038 strgdesrdaigrqdnrlrtisadamatlvgll-qrgmlvppaysavltpr 1088

ID	AY32020	standard: Protein; 1159 AA.
XX	AY32020;	
XX	05-JAN-2000 (first entry)	
XX	Human cation channel protein.	
XX	Cation channel protein; CCP; ion transport; arrhythmia;	
XX	diabetes mellitus; seizure; asthma; hypertension; therapy;	
XX	protein engineering; human.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Region	61..119
XX		/note="crystal region"
XX	W09947923-A2.	
XX	23-SEP-1999.	
XX	22-MAR-1999;	99WO-US06307.
XX	20-MAR-1998;	98US-0045529.
XX	02-APR-1998;	98US-0054347.
XX	(UTRQ ) UNIV ROCKEFELLER.	
XX	Mackinnon R;	
XX	WPI: 1999-601131/51.	
XX	Assays for screening compounds which interact with cation channel	
XX	proteins, useful for providing agents for treatment of diseases	
XX	Claim 21; Page 153-156; 165pp; English.	
XX	The present sequence represents a human cation channel protein	
XX	(CCP). The invention provides an assay for screening potential	
XX	drugs or agents which interact with CCPs using prokaryotic CCPs	
XX	(such as those given in AY32009-12) mutated, using recombinant DNA	
XX	technology, to mimic the physiological function and chemical	
XX	properties of a functional eukaryotic CCP (such as those given in	
XX	AY32013-22). An example of a mutated prokaryotic CCP is given in	
XX	AY32024. The crystal region of the CCP may also be used in the	
XX	assay. The drugs or agents obtained can be used to treat	
XX	conditions related to the function of CCP in vivo, such as cardiac	
XX	arrhythmia, diabetes mellitus, seizure disorder, asthma or	
XX	hypertension. The invention has overcome the physical limitations	
XX	regarding the isolation and purification of eukaryotic CCPs.	
XX	Sequence: 1159 AA;	
XX	Query Match	28.3%; Score 1415; DB 20; Length 1159;
XX	Best Local Similarity	30.1%; Pred. No. 5.8e-122;
XX	Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps	28
XX	7 RRGGLVAPONTFLENIVRR--SNDTNEVLGNAQIVDPPIVYSNDGCKLSGYHRAEYMOKS	64
XX		
XX	4 rrgvhpapntfidtlirrfegskrfllanarvencavlyncdgcfcclgyraetmmp	63
XX	65 STCSMNGELDPKDTIEKVRQTFEYENANSFELMKKNTPTWFFVKIAPIRNEQDKV	124
XX		
XX	64 ctcdclhlpbtrtgraaagagallgaerkyelafyrxdgscfcldvdpvknedgavl	123
XX		
XX	125 LFLCTFS-----	131
XX	124 mflinfvewmekdmvgsphdtnhvgpptswlapapraktfrliklpallaltarassvsg	183

OY	132	-----DITAKQPIE-----	-----DDSGKMGKFRRLAL-----	158	
Db	184	gaggaagagvavvdvdltpaapsesialdevtamdhvagiipr	aeerlaltvpgpsppr	242	
OY	159	-----TSSR-----	-----GVL-----	165	
Db	243	sapgdpsprahsinpaagscsalartrescasvrrassaddlemragvlpprrph		302	
OY	166	-----	-----OOLAPS	171	
Db	303	astgamhplfsgllnsdsedlvrryrltskfpqcltnfvdlkxgdpflaprsdrelaprk		362	
OY	172	VQKEENVHK-HSRLEAVLLOSDILOPOYKQEKAPKTRPHIIILHYCVKTTWMDIILILFY		230	
Db	363	lk--erthnvtckvtqvislqadavlpeyklqaprlhrwtlhyssprkavwdvllilvly		420	
OY	231	TAILVPYNVSEFKTRONNVA-----	-----WLVDSDIVDFVLVDVLFVNFPTTFVCPAG	278	
Db	421	tavtprysaafllketecegpatecygaacplavdlvldimfvdlilnfttyuane		480	
OY	279	EVISDPKLIRANNVKTWFIIDLLSCLEPYDINA.FENVDBGISLSSFLSKVRLRYGVA		338	
Db	481	evshpripriavhyfkgywfilidmvaalpfdll-----	lfgsgseellglkltarllrlvrva	536	
OY	339	RKLDHYIEYGAAYVILVYCPGLAAHMCIMWSICDYEIPDEDKTITNNMWLQOLAMD		398	
Db	537	rkldryeygaavafllimctfialahlaeiwaylismeqphndrl-----	gwlhnlqdg	592	
OY	399	IGTFYQNGSGSGKMEGPGKNSVYSLSLFTWTSLTSGVGNIASTDIEKIFPAVAM		458	
Db	593	lgkry--nsagl-----	ggpalkkkytalvlyftsltsvsgfngvprntseklfscvml	646	
OY	459	IGSLVATTFGNVTTTITQOMANTNRYHEMLNSRDFLKLVOYRKLGSFEMDYIVSTWS		518	
Db	647	lgslymasifgnvsailqrlrlysgtaryhtcmrlvrrefifhqlpmlrqrlleeyfqhaws		706	
OY	519	MSRDIPEKYLQICPKMRKADICVHNIRKRYKFKHNAFRLASGSCBALAMEQOTYHACG		578	
Db	707	ylngldimavaylqfpeclqadclhlnrslilqhcprkfaytckyltalamkfkltthaprg		766	
OY	579	DLIHAGEVSDFCLFVVGSGLEVITODENVALIGKDDVGDGFWMKEATLQSCANVRLT		638	
Db	767	dtlvahgdlltalvylfsgstlcllrgdvvaallqkndifgerlnlyatprgksngdvrlt		826	
OY	639	YCDLHVIKRDALQVLEFYTAFSHSFRNLILTYNLKRKIVFRKISDYVKEEBEEMKRN		698	
Db	827	ycdlhhkthrddllevlmdyefadhfwsletfllnr-----	dtl-----	866	
OY	699	EAPLILRPDHPVRKRLRFRFOQOEAKRLAERGRDLDLDVKEGNVLTHNASANISLYKA		758	
Db	867	---mlpgspgstelqegvifsgqrkrlstfr-----	ftldcteq-----	901	
OY	759	SVMTVRESPATPVSFQAASTGVPRDMAKLOAPSECLCGKGGGDOCAKKRSMARFKDCG		818	
Db	902	-----	-----pgevsaigpragagpsstg-----	trpgrgv	928
OY	819	KSEDMNVKSAESMETLIPERTKA-----	-----SGEATL-----	KKTDCD----	854
Db	929	espspgsspressedegprgsssplrlvprfssprppgdepprgplmedceksdcpnls		988	
OY	855	-----SGITKSDLRLDNV-----	GEARSPQ-DRSPILAEVKSFTFPRBQTLQATVLEVRHEL	906	
Db	989	gafgsvs-----	nlfsfwgdrgtgrgyqelprcpaprpallnlp-----	lsspgtrpgrdv	1038
OY	907	KEDIKALANAKMTNIEKOLS-----	EILRIILTSRSSGSPQELREISRP	949	
Db	1039	esrldalqrlnrlctrlsadmavtqlql-qrgmclvppaysavtlpr		1084	



AAV85405;  
 20-JUN-2000 (first entry)  
 Long QT syndrome associated HERG protein.  
 HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human.  
 Homo sapiens.  
 Key location/Qualifiers  
 Misc-difference 572 /note= "can be substituted with Cys; specifically claimed"  
 Misc-difference 588 /note= "can be substituted with Asp; specifically claimed"  
 Misc-difference 614 /note= "can be substituted with Val; specifically claimed"  
 Misc-difference 630 /note= "can be substituted with Ala; specifically claimed"  
 WO200006772-A1.  
 10-FEB-2000.  
 20-JUL-1999; 99WO-US16337.  
 27-JUL-1998; 98US-0122847.  
 06-JAN-1999; 99US-0226012.  
 (UTAH ) UNIV UTAH RES FOUND.  
 Keating MT, Splawski I;  
 WPI: 2000-195319/17.  
 N-PSDB: AAA07601.  
 New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome  
 Claim 11; Fig 8A-B; 163pp; English.  
 The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and HERG peptides can be used for peptide therapy. The present sequence represents the LQT syndrome associated HERG protein. The HERG protein gene sequence comprising any of the following mutations apart from those indicated above is also specifically claimed for in the specification. The mutations arise from specific alterations in the encoding HERG gene sequence. The mutations can be F29L, N33T, C44Stop, G47V, G53R, R56Q, C66G, H70R, P720, R73frameshift, A78P, A83frameshift, O81Stop, L86R, P111frameshift, P151frameshift, P241frameshift, V285frameshift, R312C, P347S, R310Q, L552S, A561T, G584S, W585C, I593T, G604S, D609N, T613W, L615V, G626S, F627L, P632S, K638E, G61K638, M645L, E682SStop, H799frameshift, R752W, I798frameshift, F805S, F805C, R823W, N861I, H866frameshift, P917L, R920frameshift, R922W, G925frameshift, P968frameshift, P968frameshift, W1001Stop, R1014Stop, G1031frameshift, and P1101frameshift.  
 Sequence 1159 AA;

Query Match 28.3%; Score 1415; DB 21; Length 1159;  
 Best Local Similarity 30.1%; Pred. No. 5,8e-122;  
 Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps 28;

7 RRGVAPONTFLENIYVR--SDNTNFEVLCNAQIVDPPIYSNDGFECKLSGARAEVQKS 64  
 4 trghvapnctffiditirkfegsirkflianarvencavlycndfcelegrsraewmqrp 63  
 65 STCSFMYGELTDKDTLEKROTFEENEMSFELAMKKKRTPVWFVXKAPINBEDKXV 124  
 64 cctcdifhprlqtraaaglaqallgaerkevlatyrkdgscfclvdvpxknedgav1 123  
 125 LFLCTFS----- 131  
 124 mfilnfvevmekdwgspahdchnrgpptsxlapgraktfrllpallataressvsg 183  
 132 -----DITAFKQPIE-----DDSGKMGKFARLTRAL----- 158  
 184 gagagagapavvvvdvlltpaapsesaldevlamdhvagiap-aeerallvgpspr 242  
 159 -----TSSR-----GVL----- 165  
 243 sapqqlpsprahslnpdasgssclartrescasvrrassaddleamragvlppprh 302  
 166 -----QDLAPS 171  
 303 astgambplrsgllnstdsdlvrytliskipqitlnfvdlkqdpfiaspsdreliapk 362  
 172 YQGENVNR-HSRLEAVLQSGDILPQYKQEARPTPHILHYCVKRTWDWIIILTFY 230  
 363 IK--erthnvtelvtqlslgadvlpeykqaprlhwllhyspfkavdwvllllyv 420  
 231 TALVPYVNSFKTRONVA-----WLVDSYDVVITLVQIVLNFHTTFPGPAG 278  
 421 tavlfrysaafllketeegppatecgcyaqplavvdldvdmivlilnfrityvname 480  
 279 EVISDPLIRMYNLKTFPIYDLSCPYDPIYNAFENVNDEGISLSFSLKVRLLRGVA 338  
 481 evshpgrlavihvfkgwflldmvaalpfidll----ifsgseeliglkarllirvra 536  
 339 RKLHYIEYGAVALVLCVFGFLAHHMACIWSIGDYELFDEDTKTRINNSMLYOLAMD 398  
 537 rkldrysegaavllfmetfaliahwaciawalgaimeqphmdst----gvlhmgdq 592  
 399 IGPYPFNGSGCKMGCKGSKNSVYISSLYFTMTSLTSVFGNIASTDEKIFNAIIM 438  
 593 lqkpy--nssgl---ggsikdkyvtalyftfsltsvfgnpsphtseklfscvml 646  
 459 IGSILYATIFGNVTTIFQOQVYANTNRYHEMLNSVDPFLKLYQVPGKLSRVNDYISTVS 518  
 647 lgsilmastfgnvsalqtrlysgtarlyhcmlyrelirhqlpmlrgrllyefghaws 706  
 519 MSRGIDTEKVALQICPKMRADICVHLNRKVEKHPAERLASDCLRALAMEFOTVHCAPG 578  
 707 ytingidmanavlkqfpeclqgdclhlnrsllhnockprfgatkgclralamkftltharp 766  
 579 DLIVHAGESVDSLCFVSGSLEVIQODEVVAIIIGKGVPEQEDVWKEKTTALQSCANPAL 638  
 767 dclvhagdlitalyflsrgstlellrgdvvaalqgkndilgepnllyarpqksngdvait 826  
 639 YCDLHYIKDALQVLEFYAFSHSFRNLILTYNLKRLIVFRKISVYKREERBMKRN 698  
 827 ycdlhihnddllevldmpefdhfwssleifnl-----dtn----- 866  
 699 EAPLIPPHVPRRLPQRFROKREARLAERGRDLDLVERGMVLTETHASANSLVKA 758  
 867 ----mipsgpsstelagsgfgrkrksfr-----rdkdeq----- 901  
 759 SVTVRESAPTPVTSFOAASGVPDHAKLQAPGSECLGPRGGGDCAKKRSMAFKDAG 818  
 902 -----pgevsaigpragagpsrg-----tpgpgw 928  
 819 KSEDMNKVSKAESMFTLPERTKA-----SGEATL-----KKTDSO--- 854  
 929 espsspspsessedegprssplrlvfpssprppgpggelmedckssstclmpls 988  
 855 ---SGITKSDLRLDNV---GEARSPO-DRSPILAEVKAHSFVPIPEOTLQATVLEVHNL 906



DT 04-MAY-2000 (first entry)  
 XX Human Elk voltage gated potassium channel monomer variant #3.  
 XX Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;  
 KM Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;  
 KM Chromosome 12q13; resting potential; cell excitability; seizure; marker;  
 KM CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;  
 \* ion flux disorder; reporter molecule; detection; gene therapy;  
 \* ion flux disorder; reporter molecule; detection; gene therapy;  
 KM antimigrane; cerebroprotective; neuroprotective; antipsychotic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Region 452..514  
 FT /label- P-S6\_region  
 FT /note- "Pore-S6 region with conserved amino acids"  
 FT Region 452..710  
 FT /label- Extended\_P-S6\_region  
 FT /note- "Extended Pore-S6 region with conserved amino acids"  
 FT Misc-difference 744  
 FT /note- "Wild type Ala substituted with Ser"  
 FT  
 XX  
 PN WC200001819-A1.  
 PD 13-JAN-2000.  
 XX  
 PE 30-JUN-1999; 99WO-US14944.  
 XX  
 XX 01-JUL-1998; 98US-0091469.  
 PR 21-JAN-1999; 99US-0116621.  
 XX  
 PA (ICAG-) ICAGEN INC.  
 PI Jegla TJ, Wickenden A;  
 XX  
 DR WPI: 2000-182114/16.  
 XX  
 PT Novel polynucleotides and polypeptides of human Elk, a voltage-gated  
 PT potassium channel subunit useful for treating Elk mis-expression and  
 PT to screen for inhibitors and activators of such channels  
 XX  
 PS Disclosure: Page -: 79pp; English.  
 XX  
 CC The present sequence is the human Elk (hElk) polypeptide variant #3,  
 CC comprising an alpha subunit of the voltage-gated potassium channel  
 CC (VGPCs). It is a member of the Kv (Voltage-gated potassium) superfamily,  
 CC Eag (ether a go-go) family and Elk subfamily of potassium channel  
 CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated  
 CC from brain and maintains the resting potential and controls excitability  
 CC of the cell. It has antimigrane, cerebroprotective, antipsychotic,  
 CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be  
 CC used to screen for modulators of VGPCs, that are useful for treating  
 CC abnormal ion flux disorders, CNS disorders such as migraines, hearing  
 CC and vision problems, seizures, psychotic disorders and to prevent  
 CC strokes. It can be used as a marker for diagnosis of diseases linked to  
 CC this gene and also as reporter molecule in detection systems. The  
 CC polynucleotide is useful for gene therapy, to rectify Elk expression.  
 CC Note: The present sequence is not found in the specification but  
 CC derived from hElk amino acid sequence found in page 62.  
 XX  
 SO Sequence 1083 AA;

Query Match 27.4%; Score 1370; DB 21; Length 1083;  
 Best Local Similarity 32.7%; Pred. No. 8e-118;  
 Matches 333; Conservative 183; Mismatches 335; Indels 168; Gaps 25;

QY 8 RGLVAPONTFLENTYRSDNT--NFVLGNAQLVD-WPIYVSDGKCKLSGYRAEYMQKS 64  
 DB 5 RGLVAPONTFLENTYRSDNT--NFVLGNAQLVD-WPIYVSDGKCKLSGYRAEYMQKS 64  
 DB 5 RGLVAPONTFLENTYRSDNT--NFVLGNAQLVD-WPIYVSDGKCKLSGYRAEYMQKS 64

QY 65 STCSFMYGELTDTKDTLEKQTFEYENKNSFEILMYKKRNPVWEFVKIAPLRNEQKVV 124  
 DB 65 cacsflpdpstselvrgqtrkaldekhefkaelllyrksqglpwcldvlpknekegva 124  
 QY 125 LFLCTFSDITAKQPIEDDSCK--GNGKRALRLALTS-----SRVLDQALASVOK 174  
 DB 125 lflvskdiseekknrgpdrkwtggr--rygratskfnanrrrsravlyhlsghlqk 183  
 QY 175 GENVKHSHSLAEVLQSGDI-----LPQYKQEAFTPHIILHYCVFTTMMWILLITG 228  
 DB 184 -qpkgh-----klnkvfgekpnlpkykvaairkspfillhgalratwdgfilliat 235  
 QY 229 FYTALVPYVNSFKT--RQNNVAM--LVVDSIVDIVFLVDIVLNFHTFVGAGEVISDP 284  
 DB 236 lyvavtvpysvcvstarepsaarppsvcdlavewlflidivlnftftfvskegqvafp 295  
 QY 285 KLIRKMYLKTWVVIDLSCLPVDVYNAFENVDGJSLSS--LKVYRLRLGRVARKLD 342  
 DB 296 kslchlyvtwtvflldvialaiafpdlhahf-----vvvfygahlkltvrlrlrlprld 350  
 QY 343 HYIEGAVALVLLVCVGLAAHMAACIWSIGDEIFDEDTKTRRNNSMLYOLAMDIGTP 402  
 DB 351 rysqysavvlllmavfallahwacwvlylqgrelesese--lpeiylgelarricp 409  
 QY 403 YQF-----NGSOSGRWE-----GGPSKNSVYISLSYFTMSLTSVGRG 440  
 DB 410 yllvgrirpagnsgsdscssseangtglellgppslrsayltslyfalsltsvgfg 469  
 QY 441 NTAPSTDIEKIRAVAIMIGSLIATIFGNVTTFOOMTANTRKRYEMLSNVDFLKLQ 500  
 DB 470 nvsantdekisiccmllgalmhavfignvtairlqmyairflsrtldldyrlhr 529  
 QY 501 VPKGLSERVMDYIVSWMSRSGIDTEKVLQICPKRADICVLNKRKVEKHPAFRLASD 560  
 DB 530 lpeplkqrmleyfgatwaanngidtcellygsipdelradiamlhvcl\_qlrlfeastr 568  
 QY 561 GCLRALMEFQTVHCAPGLIYHAGSVDSLCPVSGSLEVIDDEVALIGKGVGDV 620  
 DB 589 gclralstslrpaftcpgelyllhbgdalgalyfvcsgsmvelkgvctvialllygdllgce 648  
 QY 621 FWEKATLAOSCANVRLTYTCDLVHVKRDALQKYLEYTAFSHFSRNL--ILTYNLKRI 678  
 DB 649 lpreqvvkanadvkgltycvlqclqaglhdslalyelapaftrfsglylgelesyn----- 703  
 QY 679 VPEKISDVKREEBERMKRKNKNEAPLILPDHPVRLRQRFQKQEARLAARGRDLD 728  
 DB 704 -----lgaggsaeavdts 717  
 QY 739 VEKGNVL--TEHASANHSLVKASVYTVRESPTVPSFOASTSGVPDHAQLQAPSECL 795  
 DB 718 lsgdtlmstleeketdeggeqrvpspadepsspllspctclass--saakllsprrtap 775  
 QY 796 GPKGGGDCAKKRSARFKDACKGSEDMNKVSKAESMETLPERT-----K 840  
 DB 776 rpllggrgrrpgrag-----alkaagsapralaqglrlpmpmwvppd 819  
 QY 841 ASGEATLKKTDCSDGSTRKSDRLDNVG-----EARSQDSSPLAEKHSFYRIPRGTIQ 896  
 DB 820 lsrvtvvgiedgsgsqpkstfvgsgspccsspgypesgillt-----vphgpe 871  
 QY 897 ATYLEVRHEHLEKEDIKALNAKMTNIEKOLSEILR-----ILTSRRSSQSPQELFEISRPQS 951  
 DB 872 arntdtldklrgevtselsegvlgmreglqslrgavqlvlabphregpcprassgpgcpas 930

RESULT 12  
 AAY22427  
 ID AAY22427 standard; Protein; 1017 AA.  
 AC AAY22427;  
 XX  
 DT 28-SEP-1999 (first entry)







FT	Modified-site	129..131	/note="Protein kinase C phosphorylation site"
FT	Modified-site	150..152	/note="Protein kinase C phosphorylation site"
FT	Modified-site	250..252	/note="Protein kinase C phosphorylation site"
FT	Modified-site	336..338	/note="Protein kinase C phosphorylation site"
FT	Modified-site	447..449	/note="Protein kinase C phosphorylation site"
FT	Modified-site	477..479	/note="Protein kinase C phosphorylation site"
FT	Modified-site	769..771	/note="Protein kinase C phosphorylation site"
FT	Modified-site	821..823	/note="Protein kinase C phosphorylation site"
FT	Modified-site	840..842	/note="Protein kinase C phosphorylation site"
FT	Modified-site	901..903	/note="Protein kinase C phosphorylation site"
FT	Modified-site	13..16	/note="Protein kinase C phosphorylation site"
FT	Modified-site	20..23	/note="Protein kinase C phosphorylation site"
FT	Modified-site	56..59	/note="Protein kinase C phosphorylation site"
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FT	Modified-site	475..478	/note="Protein kinase C phosphorylation site"
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FT	Modified-site	726..729	/note="Protein kinase C phosphorylation site"
FT	Modified-site	733..736	/note="Protein kinase C phosphorylation site"
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FT	Modified-site	1040..1043	/note="Protein kinase C phosphorylation site"
FT	Modified-site	1076..1079	/note="Protein kinase C phosphorylation site"
FT	Modified-site	404..411	/note="Tyrosine kinase phosphorylation site"
FT	Modified-site	517..524	/note="Tyrosine kinase phosphorylation site"
PN	WO200005346-A1.		
PD	03-FEB-2000.		
PF	21-JUL-1999;	99WO-US16752.	
PR	21-JUL-1998;	98US-0119855.	
PA	(MILL-) MILLENNIUM PHARM INC.		

[illegible]

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Page 17

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Oy      621 FMKEATLAOSACANBALYQCDHVIKRDALOKVLEFPTAASHSSRRL--ILTYNLAKRI   678
Db      649 lprreevvaknadqkyllycvclgcqlaglnslasialypelaprtgrlrgelysn-----  703031
Oy      679 VFRRKISDVKKREEEERMKRKNEAPLTPPDHPVRLLFORFRookeEARLaERGSDLDLD    738
Db      704 -----lgagggsaeavtss 717

Oy      739 VEKGNYL--TEHASANHLYKASVTWRESPATPVSFOAASTSGVDPAHKLAOPGSECL   795
Db      718 lsgdnlmstleeketdegpgptvspadepssllspgctsss--saakllsprtrap     77571
Oy      796 GPKGGGGCARKKRSMARFKDCKGSSEDNMKYSKAESMETLPERT-----K 840
Db      776 rprlrgrgrprag-----alklaeagsaprprieglrlrppmwrvpvd 819

Oy      841 ASGEATLKKTSCSGICRTSDDLNDNG---EARSQODRSPLAEVKHSFYRPEDTLO 896
Db      820 lsprvvdgiedcgsgdqpklsfrmgqspeccsspspqseglit-----vrhpse    87171

Oy      897 ATTVLEVREHLKEDIKALKAMNTNIEKOLSELRL----ITLSRSSQSPOELFEISRPOS 951
Db      872 arnndtlcklqgamelsavgilmregqlsrqdvqlaplaphreogpcrrsgsgpcpas 930
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RX MEDLINE=971176600; PubMed=9024139; Takata S., Yano K., Yabuta K.,  
 RA Tanaka T., Nagai R., Tomoiike H.,  
 RA Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,  
 RA Nakamura Y.,  
 RT "Four novel KVLQT1 and four novel HERG mutations in familial long-QT  
 RT syndrome.";  
 RL Circulation 95:565-567(1997).  
 RN [8]  
 RP VARIANTS LOT2 CYS-572; ASP-588; VAL-614 AND ALA-630.  
 RX MEDLINE=98360095; PubMed=9693036; Vincent G.M., Lehmann M.H.,  
 RA Splawski I., Shen J., Timothy K.W.,  
 RT "Multiple different missense mutations in the pore region of HERG in  
 RT patients with long QT syndrome.";  
 RL Hum. Genet. 102:265-272(1998).  
 RN [10]  
 RP VARIANTS LOT2 SER-601.  
 RX MEDLINE=98112459; PubMed=9452080; Furutani Y., Kasanuki H.,  
 RA Akimoto K., Furutani M., Imanura S.-I.,  
 RT "Novel missense mutation (G601S) of HERG in a Japanese long QT  
 RT syndrome family.";  
 RL Hum. Mutat. Suppl. 1:S184-S186(1998).  
 RN [11]  
 RP VARIANTS LOT2 PRO-558; CYS-582; SER-604; MET-613 AND LEU-640.  
 RX MEDLINE=99235550; PubMed=10220144; Doeveendans P.,  
 RA Jongbloed R.J.E., Wilde A.A.M., Geelen J.L.M.C.,  
 RA Schaap C., Van Langen I., van Tintelen J.P., Cobben J.M.,  
 RA Beaufort-Krol G.C.M., Gerechtis J.P.M., Smeets H.J.M.,  
 RT "Novel KCNQ1 and HERG missense mutations in Dutch long-QT families.";  
 RL Hum. Mutat. 13:301-310(1999).  
 RN [12]  
 RP VARIANTS LOT2 ARG-572.  
 RX MEDLINE=99235552; PubMed=10220146; Vuust J., Andersen P.S.,  
 RA Larsen L.A., Christiansen M.,  
 RT "High-throughput single-strand conformation polymorphism analysis by  
 RT automated capillary electrophoresis: robust multiplex analysis and  
 RT pattern-based identification of allelic variants.";  
 RL Hum. Mutat. 13:318-327(1999).  
 RN [13]  
 RP VARIANTS LOT2 L-29; T-33; R-53; Q-56; G-66; R-70; P-78 AND R-86.  
 RX MEDLINE=99214566; PubMed=10187793; Sanguinetti M.C.,  
 RA Chen J., Zou A., Splawski I., Keating M.T.,  
 RT "Long QT syndrome-associated mutations in the Per-Arnt-Sim (PAS)  
 RT domain of HERG potassium channels accelerate channel deactivation.";  
 RL J. Biol. Chem. 274:10113-10118(1999).  
 RN [14]  
 RP VARIANTS LOT2 LYS-629.  
 RX MEDLINE=99445248; PubMed=10517660; Kubota T.,  
 RA Yoshida H., Horie M., Ohtani H., Takano M., Tsuji K.,  
 RA Fukunumi M., Sasayama S.,  
 RT "Characterization of a novel missense mutation in the pore of HERG in  
 RT a patient with long QT syndrome.";  
 RL J. Cardiovasc. Electrophysiol. 10:1262-1270(1999).  
 RN [15]  
 RP VARIANT LOT2 ARG-572.  
 RX MEDLINE=20197680; PubMed=1075633; Andersen P.S.,  
 RA Larsen L.A., Svendsen I.H., Jensen A.M., Kanters J.K.,  
 RA Møller M., Sørensen S.A., Sandoe E., Jacobsen J.R., Vuust J.,  
 RA Christiansen M.,  
 RT "Long QT syndrome with a high mortality rate caused by a novel G572R  
 RT missense mutation in KCNH2.";  
 RL Clin. Genet. 57:125-130(2000).  
 RN [16]  
 RP VARIANTS LOT2.  
 RX MEDLINE=20432616; PubMed=10973849;

```

RA Splanask J.L., Shen J., Timothy K.W., Lehmann M.H., Priori S.,
RA Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,
RA Keating M.T.:
RT "Spectrum of mutations in long-QT syndrome genes, KVLQT1, HERG, SCN5A,
RT KCNE1, and KCNE2."
RL Circulation 102:1178-1185(2000).
CC -1- FUNCTION: INWARDLY RECTIFYING CARDIAC POTASSIUM (IKR) CHANNEL.
CC -1- SUBUNIT: MAY ASSEMBLE WITH EITHER MIRP1 OR MINK. COMPLEXES WITH
CC MIRP1 ARE MORE STABLE.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.
CC -1- DISEASE DEFECTS IN KCNH2 IS ASSOCIATED WITH LONG QT SYNDROME TYPE
CC 2 (LQTS2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED QT SEGMENT
CC ON THE ECG AND POLYMORPHIC VENTRICULAR ARRHYTHMIAS KNOWN AS
CC TORSADES DE POINTES. THESE ARRHYTHMIAS OFTEN OCCUR IN RELATION TO
CC EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT SYNCOPES,
CC SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN ASSOCIATED TO
CC THE SYNDROME.
CC -1- MISCELLANEOUS: IT HAS THE ARCHITECTURAL PLAN OF THE
CC DEPOLARIZATION-ACTIVATED POTASSIUM CHANNEL FAMILY (6 PUTATIVE
CC TRANSMEMBRANE SEGMENTS), YET IT EXHIBITS RECTIFICATION LIKE THAT
CC OF THE INWARD-RECTIFYING POTASSIUM CHANNELS.
CC DATABASE: NAME=LQTSdb; NOTE=KCNH2 mutations page:
CC WWW="http://www.ssi.dk/en/forskning/lqtsdb/herg.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between The Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch).
CC -----
DR EMBL; U04270; AAA62473.1; -.
DR EMBL; AB009071.1; BAA37096.1; JOINED.
DR EMBL; AB009057.1; BAA37096.1; JOINED.
DR EMBL; AB009058.1; BAA37096.1; JOINED.
DR EMBL; AB009059.1; BAA37096.1; JOINED.
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DR EMBL; AB009061.1; BAA37096.1; JOINED.
DR EMBL; AB009062.1; BAA37096.1; JOINED.
DR EMBL; AB009063.1; BAA37096.1; JOINED.
DR EMBL; AB009064.1; BAA37096.1; JOINED.
DR EMBL; AB009065.1; BAA37096.1; JOINED.
DR EMBL; AB009066.1; BAA37096.1; JOINED.
DR EMBL; AB009067.1; BAA37096.1; JOINED.
DR EMBL; AB009068.1; BAA37096.1; JOINED.
DR EMBL; AB009069.1; BAA37096.1; JOINED.
DR EMBL; AB009070.1; BAA37096.1; JOINED.
DR EMBL; AJ010538.1; CAA09232.1; JOINED.
DR EMBL; AJ010539.1; CAA09232.1; JOINED.
DR EMBL; AJ010540.1; CAA09232.1; JOINED.
DR EMBL; AJ010541.1; CAA09232.1; JOINED.
DR EMBL; AJ010542.1; CAA09232.1; JOINED.
DR EMBL; AJ010543.1; CAA09232.1; JOINED.
DR EMBL; AJ010544.1; CAA09232.1; JOINED.
DR EMBL; AJ010545.1; CAA09232.1; JOINED.
DR EMBL; AJ010546.1; CAA09232.1; JOINED.
DR EMBL; AJ010547.1; CAA09232.1; JOINED.
DR EMBL; AJ010548.1; CAA09232.1; JOINED.
DR EMBL; AJ010549.1; CAA09232.1; JOINED.
DR EMBL; AJ010550.1; CAA09232.1; JOINED.
DR EMBL; AJ010551.1; CAA09232.1; JOINED.
DR MIM; 152427; -.
DR InterPro; IPR000595; -.
DR InterPro; IPR001610; -.

Query Match      28.3%, Score 1415, DB 1, Length 1159;
Best Local Similarity 30.1%, Pred. No. 1,2e+83;
Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps 28;

7 RRGVAPONTFLENIVRR--SDNTRFVLCNAOIVMPYISNDGCKSLSGHRAEVMOKS 64
   ||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
4  RGHVAPONTFLDTRIRFEFGOSKRFFIIIAANRVENCVAIVYCDNGFCCELGCSRAEVMOPR 63

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QY 65 STGSEWYGEIADKDIETKROTFFENYEMNSFEIIMYKKNRTPVWFVKIAPIRNODKV 124
DB 64 CTCEFLHGPRTQRAAAQIAQALLGAERKVEIARFKDGSOFICLVYVVPKNEGAVI 123
QY 125 LFLCTFS----- 131
DB 124 MFIIFEVWEKMDVNSPAHDTNHRPTSMWLPGRAKTFRILKLPALLATARESSVBSG 183
QY 132 -----DIFAPKQPIE-----DSCCKGKGFARLTAL----- 158
DB 184 GAGAGAGAVVVDVLTLPAAAPSESLALDEVYAMDNHVALGP-AEERRALVNGSGSPR 242
QY 159 -----TSSR-----GVL----- 165
DB 243 SAPQOLPSPRAHSLNPDASSGSLARTRRESGASVRRASSADDIEAMRGVLPPEPRH 302
QY 166 -----OOLAPS 171
DB 303 ASTGAMHPLRSGLNSTSDSLVRYRTISKIPQITLNFVDLKGDFLASPTSDREITIAK 362
QY 172 VOKGENVHK-HSRLAIEVLOGSDILPOYKOEAKRPHIILHYCVKTTWMIILITFY 230
DB 363 IK-ERTHNTERTKQVLSLGDVLPETKQAPRIHRMTILHSPFKAWMDLILLVY 420
QY 231 TAILVYVNSFKTRONNVA-----WLVDYSIVDVFYLDVILNFHTTEVGPAG 278
DB 421 TAVFPYSAAFKLTETEGSPATEGCGYACOPAVVDLVDMIFVILINFTTYVNAME 480
QY 279 EVISDPKILIRNANYLKTWVIDLSCLPYDVINAFENVDGSISSLSKYVRLGRVA 338
DB 481 EVVSHPGIIVAHYFKGWLIDVMAIPEDL---IFGSGSEELIGLKTATALLVRYA 536
QY 339 RKLBIHYEGAVALVLAVCEGLAHMAMCIWYSIGDEIPEDEKTIIRNSWMLQOLAM 398
DB 537 RKLDRISYGAVALVFLMCTFLALAHMCIWYALGNEQPMDSKI---GMLNLGDO 592
QY 399 IGTPYQFNGSGKMGEGSPKNSVYISSLYFTMTSLTSGVGNINAPSDIEKIFAVAIM 458
DB 593 IGKPY-NSSGL---GGPSIKDKYVTAIFYFSSLTSGVGNVSPNNSEKIFISICVWL 646
QY 459 IGSLLATIFGNTTIFPOOMTANTRHYHEMLNSVDFLKYOPKGLSERVMDYVSTWS 518
DB 647 IGSLLATIFGNTTIFPOOMTANTRHYHEMLNSVDFLKYOPKGLSERVMDYVSTWS 518
QY 519 MSRGIDTEKVIQICPKDMRADICVHLNRKVEHAPFALASGCRALAMEROFHCAPG 578
DB 707 YTNGLDMNAVLKGPCECLOADICLHNSLLOHCKPFRKATKGLRALAMKRTTHAPG 766
QY 579 DLIYHAGESVSLCFVSGSLEVIDDEVALILGKGVDFWKEATLAOSCAVVALYT 638
DB 767 DLIYHAGESVSLCFVSGSLEVIDDEVALILGKGVDFWKEATLAOSCAVVALYT 638
QY 639 YCDLHVIRKDALQVLEFYTAFSHSFNRLLITVNLKRRIYFRKISDYKREERERKRN 698
DB 827 YCDLHVIRKDALQVLEFYTAFSHSFNRLLITVNLKRRIYFRKISDYKREERERKRN 698
QY 699 EAPLLPDPDHVRLPFRFROCKEKLAEERGRDLDLDVKEGNVLPHASANSIYKA 758
DB 867 -----MIPSPSTELGEGFSROKRLSFR---RTKDTQO----- 901
QY 759 SVVTYRESPPATPVFOASTSGVPDHAKLOAPGSECLPKGGGDCAKRKSWAREKDACG 818
DB 902 -----PGEVSALGPRAGAPSSSG-----RGGPGWG 928
QY 819 KSEDMNKVSKAESMETLERTKA-----SGEATL---KKTDSGD--- 854
DB 929 ESPSGSPSPSESEDEGCRSSPLRLVFPSSPRPGEPEGLMEDEKESDTCNPLS 988
QY 855 ---SGITISDLRLDV---GEARSPQ---DRSPILAEVKSFPPIEPOTLOATVLEVRHL 906
DB 989 GAFSGVS-----NIFSGWDSGRROYOELPRCPAPPSLNLIP---LSSGRRPRGDV 1038

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QY 907 KEDIALNAKMTNIEKOUS-----EILRIITFSRRSSSQPELFEISRP 949
DB 1039 ESRIDLALROLNRLERLISADMAVYLOLL-QROMTLVPPAYSAVTTP 1084

RESULT 3
ID CNG_DROME STANDARD: PRT; 665 AA.
AC 024278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (CNG CHANNEL).
CN CNG.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RX MEDLINE=95045396; PubMed=7957070;
RA Baumann A., Fritts S., Godde M., Seifert R., Kaupp U.B.;
RT "Primary structure and functional expression of a Drosophila cyclic
nucleotide-gated channel present in eyes and antennae."
RL EMBO J. 13:5040-5050(1994).
CC - FUNCTION: APPROXIMATELY 50-FOLD MORE SENSITIVE TO cGMP THAN TO
cAMP. MAY BE INVOLVED IN TRANSDUCTION CASCADES OF BOTH
INTERBRATE PHOTORECEPTORS AND OLFACTORY SENSILLAE.
CC - TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.
CC - SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
FAMILY.
CC -----
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X89601; CA61760.1; -.
DR FlyBase: FBgn0014462; Cng.
DR InterPro: IPR000595; -.
DR InterPro: IPR002025; -.
DR Pfam: PF00914; CNG membrane; 1.
DR Pfam: PF00027; cAMP_binding; 1.
DR PROSITE: PS00888; cAMP_BINDING_1; 1.
DR PROSITE: PS00889; cAMP_BINDING_2; 1.
DR PROSITE: PS0042; cAMP_BINDING_3; 1.
KW Ionic channel; Ion transport; cAMP-binding; Transmembrane.
FT DOMAIN 1 110
FT TRANSMEM 111 131
FT DOMAIN 132 138
FT TRANSMEM 139 159
FT DOMAIN 160 186
FT TRANSMEM 187 207
FT DOMAIN 208 253
FT TRANSMEM 254 274
FT DOMAIN 275 325
FT TRANSMEM 326 346
FT DOMAIN 347 481
FT TRANSMEM 482 502
FT DOMAIN 503 665
FT NP_BIND 437 559
FT BINDING 496 496
FT BINDING 511 511
FT CARBOHD 135 135
SQ SEQUENCE 665 AA; 75922 MW; 9F1BDC5D9581C8DB CRC64;

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Query Match 9.4%; Score 469.5; DB 1; Length 665;  
Best Local Similarity 25.0%; Pred. No. 6; 8e-23;

Matches	165;	Conservative	110;	Mismatches	241;	Indels	143;	Gaps	22
Oy	55	YHRAEVMKSSCSGSMGELTDKOTIEKVRQFFENYENMSFEILMYKKR--TPWFEPK	112						
Db	3	HFVKAVMOSLIDSAITQOQTDPEKSSKSPALRRRLQALORLTKRRRPKPPDMLEK	62						
Oy	113	IAPINEDDKVVLFCFTESDIFAQKOPLEDSDCKGKGFARLTRALTSRGVLOQAPSV	172						
Db	63	FSNTTN-IDK-----I	72						
Oy	173	QKGENVHKHSRLAEVLQAGSDLLPOYKQEAQKTPPHILHVCVFKTMDWILILETYTA	232						
Db	73	RKGCPMEDDAALSEIR-GSSVLCNRLSVDPTLQSH-----YRLAIIV-----S	115						
Oy	233	ILVFNVSFEKTRQ-----NNVA---WLVDSDIVVILFVLVDLNFHTTFVCPAGEVISD	283						
Db	116	LAVLNIIFVVGRAVAMEWINKSAPAFWYTLDLCEFIYLLDPLVHHHEGFL-DOGLVARD	174						
Oy	284	PKLIAMNVLKT--WVIDLLSCLPQDVINAFENWDEGSSLSFLKVY---RLRLGVR	337						
Db	175	AFRLRRHIFHTKGMV-LDVLSMLPDLDAIYW-PEPTCSSLYLPCPYIVRLNRLIRNL	232						
Oy	338	ARKLD-----HYIEYGAIVLVLCVCEGLAAMMACIWSIGDEI-FDEDTKTR	387						
Db	233	WEMFRTFETANGYPAPAFICKVYLAIVLI-----HMNACWFAI-STEIGFSSD-----	281						
Oy	388	NNSWLYQLAMDIGTPYQFNGSGSGKWEQSPKSNV---YISLYFTTMSLTSVFGQNIAP	444						
Db	282	--SWYVNL-----NCTRNNTLQROYIVSFYSTLTLLTIG-ETPRP	319						
Oy	445	SDIKIFAVALMIGSLIYATIGENVTITFQOMANTNRHYEMLSNVDELKIVQPRG	504						
Db	320	ENDVYTLVVADEFLGVLIFATIVGNISMSINMNAVAREFQNRNDGVAYQVAFRRVGHE	379						
Oy	505	LSERVMDYIVSTVSSKSGIDTEKVLQICPKMDRADICVHLANKVFEKHPAFRLASDGLR	564						
Db	380	LEARIIRMFAYTWSSGSLADEERVIALALPDKAKAEIAIQVHMDTLKQVRIIFDTEGELLE	439						
Oy	565	ALAMEFQVHCAPGDLIYHAGESVDSLCPVNSGSLVETIOD--EYVAIIKGDVFQDVFW	622						
Db	440	ALVLEKLKIQVSPGDIYIKRKGDKEMKIVYKRGKLSVGGDGIYVLATLAGSVGEVSIV	499						
Oy	623	KE---ATLQSCAVNRLTYCDLHVI-KRDLQKVLEFYTAFSHSFNLLTYNLRK	676						
Db	500	LEIACNRTGNRTANVRSLGYSDFCLAKRDMETLSDYPEARSTLLTGRCOL--LRK	555						
RESULT 4									
CGNG2_RAT		STANDARD:		PRT:		664	AA.		
ID	CGNG2_RAT								
AC	Q00195;								
DT	01-DEC-1992 (Rel. 24, Created)								
DT	01-DEC-1992 (Rel. 24, Last sequence update)								
DT	01-NOV-1997 (Rel. 35, Last annotation update)								
DE	CYTLC-NUCLEOTIDE-GATED OLFACTORY CHANNEL (CYCLIC-NUCLEOTIDE-GATED								
DE	CATION CHANNEL 2) (CNG CHANNEL 2) (CNG2) (OCNC1).								
GN	CNGG2.								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
OK	NCBI_TaxID=10116;								
RN	11								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Olfactory sensory neuron;								
RX	MEDLINE=90370115; PubMed=1697649;								
RA	Dhaliان R.S., Yau K.-W., Schrader K.A., Reed R.R.;								
RT	"Primary structure and functional expression of a cyclic nucleotide-								
RL	activated channel from olfactory neurons.";								
CC	Nature 347:184-187(1990).								
CC	-I- FUNCTION: ODOURANT SIGNAL TRANSDUCTION IS PROBABLY MEDIATED								
CC	BY A G-PROTEIN COUPLED CASCADE USING CAMP AS SECOND MESSENGER.								
CC	THE OLFACTORY CHANNEL CAN BE SHOWN TO BE ACTIVATED BY CYCLIC								
CC	NUCLEOTIDES WHICH LEADS TO A DEPOLARIZATION OF OLFACTORY								

SENSORY NEURONS.

-1- SUBUNIT: HETERODIMER OF OCMC1 AND OCMC2 SUBUNITS.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: OLFACTORY NEURONS.

-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.

-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-2 IS THE INITIATOR.

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EMBL; X55519; CAA39135.1; -

DR PIR; S11517; S11517.

DR InterPro; IPR000595; -

DR InterPro; IPR002025; -

DR Pfam; PF00914; CNG\_membrane; 1.

DR Pfam; PF00027; CNMP\_Binding; 1.

DR PROSITE; PS00888; CNMP\_BINDING\_1; 1.

DR PROSITE; PS00889; CNMP\_BINDING\_2; 1.

DR PROSITE; PS0042; CNMP\_BINDING\_3; 1.

KW Ionic channel; Ion transport; GAMP-binding; Transmembrane; Multisubunit family; Olfaction.

KW DOMAIN 1 142

FT TRANSMEM 143 162 H1 (POTENTIAL).

FT DOMAIN 163 175 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 176 194 H2 (POTENTIAL).

FT DOMAIN 195 218 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 219 238 H3 (POTENTIAL).

FT DOMAIN 239 276 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 277 299 H4 (POTENTIAL).

FT DOMAIN 300 351 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 352 371 H5 (POTENTIAL).

FT DOMAIN 372 455 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 456 476 H6 (POTENTIAL).

FT DOMAIN 477 664 CYTOPLASMIC (POTENTIAL).

FT NP\_BIND 464 586 CAMP (BY SIMILARITY).

FT BINDING 523 523 CAMP (POTENTIAL).

FT BINDING 538 538 CAMP (POTENTIAL).

FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 212 212 K -> R.

SO SEQUENCE 664 AA; 76176 MW; 720806950EC27F3C CRC64;

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Query Match 8.6%; Score 432.5; DB 1; Length 664;

Best Local Similarity 25.1%; Pred. No. 1.7e-20;

Matches 144; Conservativity 98; Mismatches 227; Indels 105; Gaps 19.

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220 WDMILILTFEYALIVPVNVSFKTRONN-VAMLVVDSIVDVFPLVDVILNHTFEVGA 277

Db 145 WLFVAMPEVLYMCLLVARACEFDLGRNYFVWLVLDVDFSDVIYADLRITGFL-EQ 203

QY 278 GEVSDPKLRINNYLKT-MEYIDLSCPYDVINAFAENYDEISSLSFKVYRLRLGR 336

Db 204 GLVYDPRKLRNRYIHTLOFKLDVASIIPDLI-----YFAVGHS--PEVRNRLHFAR 257

QY 337 VARKID-----HYEYGAVALVLYCVFGLAHMMACIWSYIGDYEIFDEDTKTR 387

Db 258 MFEFDRFETRTSTYPNIFRISMLVLYIVII-----HNNACIYVYISKSIGCVDT--- 308

QY 388 NNSMLYOLAMDIGPFGYONGSGSGKMEGSPKNSVYISSLYFTMTSLNSYVCGNAPSTD 447

Db 309 ---WYPNITDPERGYLAR-----EYICLWSTLTLLTTFIG-ETPPVKD 349

QY 448 IEKIAVAIMMIGSLVATIGNTTIFQOMYANRNRRHEMNSYRDELKIQVFKGLSE 507

Db 350 EEFYLFVDFDLGLVILFATYVGNVSMISNNMATAEQAKIDAVKHTMOPFKVYSKDME 409

QY 508 RVMDIVSTWSNRGIDTEKYLQICPKDMRADICVHLNRKKYKEHPARFLASDGLRALA 567

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Db 410 KVIKFDYLMTKKTVDEREVYKLNPAKIRAEIAINVLSTLKVRITQDCEAGLLVELV 469
Oy 568 MEFQVHCAPGDLIYHAGESVDSLCFVVSGLVIODEEV--AIIKGDVGDVF---W 622
Db 470 LKLRQVSPGDIYCKRKDGKEMITIKGKLAVADGCVTYALLSAGSGEISILNI 529
Oy 623 KEATLA-OSCANVALTYCDLHVIRKDALQKYLEEFTAFSHSFRNLITVNLRRIVFR 681
Db 530 KGSKMNRRTANIRSLGYSDFCLSKDLMLEAVTEY----- 565
Oy 682 KISDYKREER-----KNEAPLIPDPHVRRLFORROCKEARLAERGR 732
Db 566 --PDAKKYLEERREILKKEGLIDENEVAASMEVD-----VOEKLEOLET----- 608
Oy 733 DLDLDVEKGNVTEHASANSHVAKASVTVRES 766
Db 609 NMDTLYTRPALLAEYTGAKQKLRKOR--ITVLET 640

RESULT 5
CNG3_CHICK STANDARD: PRT: 735 AA.
AC 090805;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE CYCLIC NUCLEOTIDE GATED CHANNEL, CONE PHOTORECEPTOR, ALPHA SUBUNIT
DE (CNG CHANNEL 1) (CNG-1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93264082; PubMed=7684234;
RA Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
RA Moiday R.S., Kaupp U.B.;
RT "Red and cone photoreceptor cells express distinct genes for
RT cGMP-gated channels.";
RL Neuron 10:865-877(1993).
CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
CC COUPLED CASCADE USING GMP AS SECOND MESSENGER. THIS PROTEIN CAN
CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE
CC PHOTORECEPTORS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
CC FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X89598; CAA61757.1; -
CC InterPro: IPR000595; -
CC InterPro: IPR002025; -
CC Pfam: PF00914; CNG_membrane; 1.
CC Pfam: PF00027; cGMP_binding; 1.
CC PROSITE: PS00888; CNG_BINDING_1; 1.
CC PROSITE: PS00889; CNG_BINDING_2; 1.
CC PROSITE: PS00890; CNG_BINDING_3; 1.
CC Ionic channel; ion transport; cAMP-binding; Transmembrane; Vision;
CC Multigene family.
CC DOMAIN 1 210 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 211 230 HI (POTENTIAL).
CC DOMAIN 231 243 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 244 262 H2 (POTENTIAL).

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FT DOMAIN 263 286 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 287 306 H3 (POTENTIAL).
FT DOMAIN 307 344 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 345 367 H4 (POTENTIAL).
FT DOMAIN 368 419 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 420 439 H5 (POTENTIAL).
FT DOMAIN 440 523 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 524 544 H6 (POTENTIAL).
FT DOMAIN 545 735 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 532 654 CAMP (BY SIMILARITY).
FT BINDING 591 591 CAMP (POTENTIAL).
FT BINDING 606 606 CAMP (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 735 AA; 85031 MW; A67ADFDD942CECE CRC64;

Query Match 8.6%; Score 437; DB 1; Length 735;
Best Local Similarity 25.9%; Pred. No. 2,1e-20;
Matches 143; Conservative 108; Mismatches 226; Indels 76; Gaps 19;

Oy 197 OKQZAPKTPPHILHYCVFKTWMIIILFPYTAIVPVYNSFKTRQ--NNVAVLVVD 254
Db 195 EOKKEVFIYIDPSSNMTY-----NMLTITAPVPYNNMCLICRACFELQIDHDKILFLD 249
Oy 255 SIYDVFIYLDIYLNFTFTVEGAGEVISDPKLRIMNYLKT-WFVIDLSCLPYDVINAEE 313
Db 250 YCSDIYVDMFVFRFTGFL-EGGLLVKDEKRLRDHYTGQVKLVDLSLPTDL--AVL 306
Oy 314 NDEGISLFFSLKAVRLRLGRVARKLD-----HIIEGAIVLVILVCVFLAAH 364
Db 307 KL--GLN--YPELRFRLRLIARLFEFFDTERTRTPYNNFRIGNLVYLII-----H 357
Oy 365 WMACIYSGIDVEIPEDEDKTIRNSMLVOLAMDICTPYQFNGSGSGKMGSPSKSVYI 424
Db 358 WNCIYFAISKVIIGFTD-----SWVP--VNSIPET--GRLSRK-----YI 395
Oy 425 SSLEYFTSLTSVGFQGNIASTDIKIFAVAIMISLTYATFGVNTTIFQOMYANTNR 484
Db 396 YSLYWSLTLLFTIG-ETPPVKNDEYLFIYIDLVGLVLFATIVGVNGSMISNNNSRAE 454
Oy 485 YHEMLNSVDFLKYVPPKGLSERVMDIYVSWMSGRGIDTEKVIQICPKMRADICVHL 544
Db 455 FOAKVDISIOYMFRRVYTDLEARVIMFDYLTNKKYVDEKCVLNLPDKLAELAINV 514
Oy 545 NRRVFEHAPFLRASGCLRALAMEFOYHACAGDILYHAGESVDSLCFVVSGLVIO 604
Db 515 HDTLKKVRIFDCEAGLLIEVLKLPYFSPGDYICKGDIIGREKVIYIKESKLAVAD 574
Oy 605 DEYV--AIIKGDVFGDVFWKEATLAOS-----CANVALTYCDLHVIRKDALQKYLEEFT 658
Db 575 DGIQFVVLSDSYFGEISILNKGSKGNRRRTANIRSLGYSDFCLSKDLMLEALTEYR 634
Oy 659 ARSHSF--SRNLTLYNLNKKRIYFKRISDYKREERKRRKNEAPLIPDPHVRRLQ 715
Db 635 EAKKALEERGRQILMKDNLIDEEARAGADPK-DLEEKIDRLTETALDTL----- 682
Oy 716 RFRQKEARLAE 728
Db 683 ---QTRFARLLAE 692

RESULT 6
CNG3_BOVIN STANDARD: PRT: 706 AA.
AC 029441;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL 3 (CNG CHANNEL 3) (CNG-3)
DE (CNG3).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia,Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94211295; PubMed=7512693;
RA Weyand I., Godde M., Flings S., Weiner J., Mueller F., Altenhofen W.,
RA Hatt H., Kaupp U.B.;
RT "Cloning and functional expression of a cyclic-nucleotide-gated
RT channel from mammalian sperm.";
RL Nature 368:859-863(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94224768; PubMed=8170936;
RA Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Mucke M.,
RA Plocherz V., Hofmann F.;
RT "Another member of the cyclic nucleotide-gated channel family,
RT expressed in testis, kidney, and heart.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509(1994).
CC -1- FUNCTION: COULD BE RESPONSIBLE FOR CGMP-INDUCED CALCIUM ENTRY IN
CC CELLS OTHER THAN SENSORY CELLS. MIGHT BE INVOLVED IN CHEMOTAXIS OF
CC SPERM.
CC -1- SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CN4 IN
CC VITRO.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: TESTIS, KIDNEY, RETINAL CONE, AND HEART.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
CC FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X89600; CAA61759.1; -.
DR EMBL; X76485; CAA54023.1; -.
DR InterPro; IPR000595; -.
DR InterPro; IPR002025; -.
DR PFam; PF00914; CNG_membrane; 1.
DR Pfam; PF00027; CNMP_binding; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW Ionic channel; Ion transport; cAMP-binding; Transmembrane;
KW Multigene family.
FT DOMAIN 1 187 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 188 207 H1 (POTENTIAL).
FT DOMAIN 208 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 239 H2 (POTENTIAL).
FT DOMAIN 240 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 283 H3 (POTENTIAL).
FT DOMAIN 284 321 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 322 344 H4 (POTENTIAL).
FT DOMAIN 345 396 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 397 416 H5 (POTENTIAL).
FT DOMAIN 417 500 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 501 521 H6 (POTENTIAL).
FT DOMAIN 522 706 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 509 631 CAMP (BY SIMILARITY).
FT BINDING 568 568 CAMP (POTENTIAL).
FT BINDING 583 583 CAMP (POTENTIAL).
FT CARBOXY 426 426 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 706 AA; 81132 MW; F499DDCD29B56239 CRC64;
Query Match 8.6%; Score 429; DB 1; Length 706;
Best Local Similarity 23.4%; Pred. No. 3;le-20;
Matches 146; Conservative 128; Mismatches 245; Indels 104; Gaps 21;

```

QY	173	OKGEVHSHSLAEVLQSGDILPOYKOEAKTPPHILHICVEKTEKTMWVILLLFTYA	233
Db	163	EKKENPKKEE-----KKDSVYMDPSSMY-----HMLYIANPVYTNW	207
QY	233	ILVPVNSFKTRÖNN--VAMLVDVSDVDFVLVDVLNFTTEVGPAGEVISDPKILRMN	290
Db	203	CLLVCRAFCEDELQSEHMLMTLVDSADILTGMDMLVARTGF--EDGLMWADASRLMKH	261
QY	291	YLKT-WFVIDLLSCLPVDVIAFENVDEGISLSFSSLLKVYLLRLGVARKLID-----	344
Db	262	YTGTLHFELDLVLSLPVDL--AYFKL--GMN--YPELRFNLLKLARLFEFEDTETFTN	315
QY	343	--HYIEYCAALVLVLVCFCGLAAMMACINVSIDYELFEDFTKTRINNSMLYOLAMDIG	400
Db	316	YPNRFRIGNLVLYILIIII-----HNNACIYAIKSLFGFGID-----SWVP---NVS	366
QY	401	TPYQFNSSGSGKMEGSPKNSVYISSLYETMTSLTSVGFNIAIDSTIEKIFAVAIMIG	466
Db	361	NPEY--GRLSRK-----YISLWSTLFTLTIG--ETPPVPVKDEEYLFVVIDFLVG	407
QY	461	SLVATIFGNVTTIFQGMVANTNTYHEMLNSVROFLKYQYQPKLSERYMDYIYSTWSMS	522
Db	408	VLIRATIVGNVSGMISNNNASRAEFQAKIDISKQYMQRYKTKDLETRVIMWEDYLMANK	467
QY	521	RGIDTEKVLQICPMDRADICVHNLRKVEKHPAPRIASDCLALAMEFQTVACAPGDL	580
Db	468	KTVDEKEVLKSLPKRLKAEIINVHLDLRLVRIFQDCEAGLIVELVUKLRPAVFSQDY	522
QY	581	IYHAGESVDSLCEPVVSGSEVYIQDEEV--AIIKGDVFGDVFKKATLAOS---CANV	633
Db	528	ICKKGDIGIREMYIIEKGKLAVVADGIGTFVLDGVSFGFISILINIKSGSKSGRRRTANI	587
QY	635	RALYVCDLHVYKRDALOKVLEFYTAFSHF---SRNLIITYNLKRRIYFRKISPVKREE	692
Db	588	RSIGTSDLEFCISKDDIMALETEYPAKKALEKRGQIIMKNDLIDELAKAGAPKIDEE	644
QY	692	--ERMKRKNRAPLILPDHPVRLLEQRFROQKEARLAAERGGRLDDLDEKGNVLTENA	745
Db	648	KVEHLETSLDS-----LQRRFARLLAEYNATQMK-----VKQRL	681
QY	750	SANHSIVKASVYVYRESPATVYS	772
Db	682	SOLESQVVMGLPPDGADPQTAS	704
RESULT 7			
CNG2_RABIT	ID	CNG2_RABIT	STANDARD; PRT; 664 AA.
AC	Q28718;		
DTA	01-NOV-1997 (Rel. 35, Created)		
DTT	01-NOV-1997 (Rel. 35, Last sequence update)		
DTF	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	CYCLIC-NUCLEOTIDE-GATED OLFACTORX CHANNEL (CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 2) (CNG CHANNEL 2) (CNG-2) (CNG2) (AORTA CNG CHANNEL) (RACNG).		
DE	CNG2.		
GN	CNGC2.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
CC	Mammalia: Euthera: Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RA	SEQUENCE FROM N.A.		
RP	TISSUE=Aorta;		
RC	MEDLINE=93359035; PubMed=7689061;		
RT	Biel M., Altenhofen W., Hüllin R., Ludwig J., Freichel M.,		
RT	Flockerzi V., Descal N., Kaupp U.B., Hofmann F.;		
RT	"Primary structure and functional expression of a cyclic nucleotide-		
RT	gated channel from rabbit aorta.";		
RT	FEBS Lett. 329:134-138(1993).		
CC	-1- FUNCTION: ODOURANT SIGNAL TRANSDUCTION IS PROBABLY MEDIATED		
CC	BY A G-PROTEIN COUPLED CANCASCADUE USING CAMP AS SECOND MESSENGER.		
CC	THE OLFACTORX CHANNEL CAN BE SHOWN TO BE ACTIVATED BY CYCLIC		



CC NUCLEOTIDES WHICH LEADS TO A DEPOLARIZATION OF OLFACTORY  
 CC SENSOR NEURONS.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, X59668; CAA42201.1; ALT\_INIT.  
 CC InterPro: IPR000595; -  
 CC InterPro: IPR002025; -  
 CC Pfam: PF00914; CNG\_membrane; 1.  
 CC DR Pfam: PF00027; CNG\_binding; 1.  
 CC DR PROSITE: PS00888; CNG\_BINDING\_1; 1.  
 CC DR PROSITE: PS00889; CNG\_BINDING\_2; 1.  
 CC DR PROSITE: PS00442; CNG\_BINDING\_3; 1.  
 CC KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;  
 CC Multigene family; Olfaction.  
 CC FT DOMAIN 1 140  
 CC FT TRANSMEM 141 160  
 CC FT DOMAIN 161 173  
 CC FT TRANSMEM 174 192  
 CC FT DOMAIN 193 216  
 CC FT TRANSMEM 217 236  
 CC FT DOMAIN 237 274  
 CC FT TRANSMEM 275 297  
 CC FT DOMAIN 298 349  
 CC FT TRANSMEM 350 369  
 CC FT DOMAIN 370 453  
 CC FT TRANSMEM 454 474  
 CC FT DOMAIN 475 664  
 CC FT NP\_BIND 462 584  
 CC FT BINDING 521 521  
 CC FT BINDING 536 536  
 CC FT CAROAMD 379 379  
 CC SEQUENCE 664 AA: 76205 MW: 5E9170D0B322B3E9 CRC64;  
 CC  
 CC Query Match 8.5%; Score 427.5; DB 1; Length 664;  
 CC Best Local Similarity 24.6%; Pred. No. 3.5e-20;  
 CC Matches 141; Conservative 99; Mismatches 228; Indels 105; Gaps 18;

DB 468 LKLRPOVSPGDYICRKGIDGKEMYYIIKEKRLAVVADGVTOYALLSAGSCFEISILNT 527  
 QY 623 KEATFLA-QSCANRALTYCDLHYIKRDAIOKYLEFYAFSHSPSRNLIITYNLRKRIVFR 681  
 DB 528 KSGKMGKRRRTANIRSLGYSDFCLSKDDIMEAVTEY----- 563  
 QY 682 KISDVREERER-----MKR-----KNEAPLILPDHVRRLFORROKEARLAEGRGR 732  
 DB 564 --PDAKVKLEERREILMKGGGLDENEVASMEVD-----VQEKIKOLET----- 606  
 QY 733 DLDLDVKGNVLTETIASANHSYKASVTVRE 765  
 DB 607 NMETLYTRFGRLAEYGAOQKLKOR--ITVLE 637  
 CC  
 CC RESULT 8  
 CC CNG2\_BOVIN STANDARD; PRT; 663 AA.  
 CC ID CNG2\_BOVIN  
 CC AC 003041;  
 CC DT 01-JUL-1993 (Rel. 26, Created)  
 CC DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 CC DE CYCLIC-NUCLEOTIDE-GATED OLFACTORY CHANNEL (CYCLIC-NUCLEOTIDE-GATED  
 CC CATION CHANNEL 2) (CNG CHANNEL 2) (CNG-2) (CNG2).  
 CC GN CNG2.  
 CC OS Bos taurus (Bovine).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC OC Bovidae; Bovinae; Bos.  
 CC OX NCBI\_Taxid=9913;  
 CC RN 11  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Olfactory epithelium;  
 CC RX MEDLINE=91032022; Pubmed=1699793;  
 CC RA Ludwig J., Margalit T., Eismann E., Lancet D., Kaupp U.B.;  
 CC RT "Primary structure of CAMP-gated channel from bovine olfactory  
 CC epithelium";  
 CC RL FEBS Lett. 270:24-29(1990).  
 CC CC -1- FUNCTION: ODORANT SIGNAL TRANSDUCTION IS PROBABLY MEDIATED  
 CC BY A G-PROTEIN COUPLED CASCADE USING CAMP AS SECOND MESSENGER.  
 CC THE OLFACTORY CHANNEL CAN BE SHOWN TO BE ACTIVATED BY CYCLIC  
 CC NUCLEOTIDES WHICH LEADS TO A DEPOLARIZATION OF OLFACTORY  
 CC SENSOR NEURONS.  
 CC CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC CC -1- TISSUE SPECIFICITY: OLFACTORY NEURONS.  
 CC CC -1- MISCELLANEOUS: THE OLFACTORY CHANNEL IS ACTIVATED BY BOTH CAMP AND  
 CC CGMP AT SIMILAR CONCENTRATIONS, WHEREAS THE CGMP-GATED CHANNEL IS  
 CC MUCH LESS SENSITIVE TO CAMP.  
 CC CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC CC -----  
 CC EMBL, X55010; CAA38754.1; -  
 CC DR PIR: S11521.  
 CC DR InterPro: IPR000595; -  
 CC DR InterPro: IPR002025; -  
 CC DR Pfam: PF00914; CNG\_membrane; 1.  
 CC DR Pfam: PF00027; CNG\_binding; 1.  
 CC DR PROSITE: PS00888; CNG\_BINDING\_1; 1.  
 CC DR PROSITE: PS00889; CNG\_BINDING\_2; 1.  
 CC DR PROSITE: PS00442; CNG\_BINDING\_3; 1.  
 CC KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;  
 CC Multigene family; Olfaction; Glycoprotein.  
 CC FT DOMAIN 1 140  
 CC FT TRANSMEM 141 160  
 CC H1 (POTENTIAL).





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OY 337 VARKID-----HYIEGAVLVLYCVGLAHNMACTIWSIGDYEIEDPKTR 387
DB 258 MEEDFDETRTSYPIERISMLVLYIIT-----HMNACTIYALSKSIGRVD- 308
OY 388 NNSMELYOLAMDIGTPYOFNGSGSGKMEGPRSKNSVYISSLYFTMTSLTSGFGNIAPSTD 447
DB 309 ---WYPRNTDDEYGLAR-----EYIYCLINSTLTLLTIG-ETPPVVD 349
OY 448 IEKIFAVLIMIGSLLYATIFGNVTTIFQOMYAMNRYHEMLNSVDFKLXYOVPGLS 507
DB 350 EEFLEFIFDLGLVLFATIVGVSGSMISNMNATRAEFQAKIDAVKHVQFRKVSADMEA 409
OY 508 RVMQDIVTWSMSRGIDPEKVLQICPKMRADICVHLNKKVREHNPAPLASDGLRALA 567
DB 410 KYIKMEVLYMTKKVYDEVEVLEKLPKRAEIALNVHLSLTKKRIIPDCEAGLLVEYL 469
OY 568 MEFOVHCAFGDLIYHAGESVDSLCEVSGSLVIODDDEV---AIIIGKDVGDV- 622
DB 470 LKLRQVSPSPGYICRKGDKGEMTIYKGLAVADGVOTYALTSAGSCFEISILNI 529
OY 623 KEATLA-OSCANVRLTYCDLHVIRKDALQVLEFYTAFSHSPSRLILTYLNKRIVER 681
DB 530 KSKMGNRTGTIRSLGYSDELFCLSKDDLMFAVTEY----- 565
OY 662 KISDYKREER-----MKR-----KNEAPLILPPD-----HPVRLFORFOOKEA 723
DB 566 --PDARKVLEEGREITMEKGLDENEVASMEVDQEKLEQLETNMTLYTRF-----A 618
OY 724 RLAEERG 731
DB 619 RLAEYTG 626

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## RESULT 10

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CNG_ICTPU
ID CNG_ICTPU STANDARD: PRT: 682 AA.
AC P53934;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Olfactory neuroepithelium;
RX MEDLINE=92110008; PubMed=1370374;
RA Goulding E.H., Ngai J., Kramer R.H., Colicos S., Axel R.,
RA Siegelbaum S.A., Chess A.;
RT "Molecular cloning and single-channel properties of the cyclic
nucleotide-gated channel from catfish olfactory neurons.";
RL Neuron 8:45-58(1992).
CC -1- FUNCTION: THIS CYCLIC NUCLEOTIDE-GATED CHANNEL IS ACTIVATED
CC EQUALLY WELL BY BOTH CAMP AND CGMP.
CC -1- TISSUE SPECIFICITY: OLFACTORY NEURONS.
CC -----
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CC -----
CC EMBL: M83111; NOT_ANNOTATED_CDS.
CC InterPro: IPR000595;
CC InterPro: IPR002025;
CC Pfam: PF00914; CNG_membrane; 1.
CC Pfam: PF00027; CNGP_binding; 1.
CC PROSITE: PS00888; CNGP_BINDING_1; 1.

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DR PROSITE: PS00888; CNGP_BINDING_2; 1.
DR PROSITE: PS00442; CNGP_BINDING_3; 1.
KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KW Olfaction.
FT DOMAIN 1 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 157 H1 (POTENTIAL).
FT DOMAIN 158 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 190 H2 (POTENTIAL).
FT DOMAIN 191 218 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 219 239 H3 (POTENTIAL).
FT DOMAIN 240 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 293 H4 (POTENTIAL).
FT DOMAIN 294 311 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 312 332 H5 (POTENTIAL).
FT DOMAIN 333 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 364 H6 (POTENTIAL).
FT DOMAIN 365 682 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 455 577 CAMP (BY SIMILARITY).
FT BINDING 514 514 CAMP (POTENTIAL).
FT BINDING 529 529 CAMP (POTENTIAL).
SQ SEQUENCE 682 AA; 78020 MW; 2C78597DC2C74F75 CRC64;

```

Query Match 8.2%; Score 409.5; DB 1; Length 682;  
 Best local Similarity 24.0%; Pred. No. 5.3e-19;  
 Matches 139; Conservative 104; Mismatches 219; Indels 117; Gaps 21;

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OY 141 EDDSCRGWCKF-----ALTRALTSRGV--LQOLAPSVQKGENVHKRSLAEVQLG 191
DB 39 DDDTCELOAVTALPEPSABMLAFQORPLARLVNLVLSLR---WAKSLVTEQRP 94
OY 192 SDILPOYK-----QEAPKTPPHILHYCVKFTWD-----WI--I 224
DB 95 DSFLERFRGQANDOSAAPADAPK-----TFKEMEGVVSQSDIYYWLF 145
OY 225 LILFEYTAIIVPVNSFKTRQ--NNVAMLVDSIVDIFLVLIANHTTFVGPAGEVIS 282
DB 146 ALASLYNMIMLVARACFDQLQDENFELMVGDLVYILDCIRLRTGYL-EGGLLVK 204
OY 283 DPKLIMNLYKT-WFVIDLLSCPYDYNAFENVDEISLSFKVYRLRGRVARKL 341
DB 205 DLAKLDNVTIRLQFKLDFLSILPTELLF-----VTVYVQLRNRLRFSRMEFF 257
OY 342 DH--YIEYGAA-----VVLVLCVFGLAHNMACTIWSIGDEIPEDEPKTRNNSWL 392
DB 258 DRETETNYNARICLLIYIYIIT-----HMNACTIYALSKSIGRVD- 308
OY 393 YOLAMDIGTPYOFNGSGSGKMEGPRSKNSVYISSLYFTMTSLTSGFGNIAPSTDIEKIF 452
DB 306 Y-----SGQNK-----TISFCYVYCFYWSLTLLTIG-EMPPVYDEYVF 345
OY 453 AVAIVMIGSLLYATIFGNVTTIFQOMYAMNRYHEMLNSVDFKLXYOVPGLSERMDY 512
DB 346 VDFPLVGLVLFATIVGVSGSMISNMNATRAEFQAKIDAKKHVHFRKVRTLETYIKW 405
OY 513 IYSTWSMSRGIDPEKVLQICPKMRADICVHLNKKVREHNPAPLASDGLRALAMFOT 572
DB 406 FDLMTNKKTVYDQEVYLNKLPDKIRAEIALNVHLSLTKKRIIPDCEAGLLVEYLKLP 465
OY 573 VHCAPGDLIYHAGESVDSLCEVSGSLVIODDDEV---AIIIGKDVGDV-----FMKEAT 626
DB 466 QVSPGYICRKGDKGEMTIYKGLAVADGVOTYALTSAGSCFEISILNIQSKM 525
OY 627 LAOSCANVRLTYCDLHVIRKDAL-----QKYLE 655
DB 526 GNRRTANIRSIGYSDLCFLSKDDLMFAVTEYPAQKYLE 564

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## RESULT 11

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CNG1_RAT
ID CNG1_RAT STANDARD: PRT: 683 AA.
AC 062927;
DT 01-NOV-1997 (Rel. 35, Created)

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
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 CC  
 DR EMBL; X89599; CA61758.1; -  
 DR InterPro: IPR000595; -  
 DR InterPro: IPR002025; -  
 DR Pfam: PF00914; CNG membrane; 1.  
 DR Pfam: PF00027; cNMP binding; 1.  
 DR PROSITE; PS00888; CNGM\_BINDING\_1; 1.  
 DR PROSITE; PS00889; CNGM\_BINDING\_2; 1.  
 DR PROSITE; PS50042; CNGM\_BINDING\_3; 1.  
 KW Ionic channel; Ion transport; cAMP-binding; Transmembrane; Vision;  
 KW Multigene family.  
 FT DOMAIN 1 117 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 118 137 H1 (POTENTIAL).  
 FT DOMAIN 138 150 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 151 169 H2 (POTENTIAL).  
 FT DOMAIN 170 193 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 194 213 H3 (POTENTIAL).  
 FT DOMAIN 214 251 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 252 274 H4 (POTENTIAL).  
 FT DOMAIN 275 326 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 327 346 H5 (POTENTIAL).  
 FT DOMAIN 347 430 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 431 451 H6 (POTENTIAL).  
 FT DOMAIN 452 645 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 439 561 CAMP (BY SIMILARITY).  
 FT BINDING 498 498 CAMP (POTENTIAL).  
 FT BINDING 513 513 CAMP (POTENTIAL).  
 FT CARBOHYD 377 377 N-LINKED (GLCNAc... (POTENTIAL).  
 SQ SEQUENCE 645 AA; 74778 MW; 989D515F61AC7D31 CRC64;  
 Query Match 8.1%; Score 405.5; DB 1; Length 645;  
 Best Local Similarity 22.9%; Pred. No. 8.9e-19;  
 Matches 135; Conservative 119; Mismatches 231; Indels 105; Gaps 20;  
 QY 199 KQKAKTPPHII-----LHYCVFKTWMIILITFYTAIIVPNYSFKTRQNN--VANA 251  
 DB 99 KEEKKKDIIFIIDPAGNMYY-----NMLEFCITMPVWYNTMTIIRACFDELANDYLAWF 153  
 QY 252 VDSIIVDVFILVDIVLNFPTTFVGPAGEVISDPKLRMYLKT-WFVIDLSCLPYDVIN 310  
 DB 154 IYDYISDYIYIADMVRYRTGYL-EGGLLVKEQKLEKTKKSLQPKIDPLIIPDL- 211  
 QY 311 AENYVDEGISLSSLSKLVVRLRLGRVAR-----KLDSYIEYGAVALVL 355  
 DB 212 YRK-----LGLNYPRLIRNRLRVAMFEFQETRTNYVPIFRISNLVWY-----IVII 262  
 QY 356 VCVFGLAHMAMACIMYSIDYIEFDEDTKTIRNSWLVLQALMDIGIPYFNGSGSKWEG 415  
 DB 263 I-----HMNACVYYSISKAIQFGADT-----WVY----- 286  
 QY 416 GPSKN-----SVYISLYFTMTSLSVGNGNAPSVDIEKIFAVAIMIGSLYAT 467  
 DB 287 -PNTSHPEPARLTKRYVSLYIMSTLITITIG-ETPPPVADSEFFVVDVLGVLFAT 344  
 QY 468 FGNVTITFOQMYANTNRHYEMLSVBDPLKLYQVPGKLSERVADYIVTWSMGRGIDTER 527  
 DB 345 VGNVSGMISNMNAARAEPQAKIDAIKQYHFRNVSKDMKRVAKWPDYLTWKNAVDERE 404  
 QY 528 VQIQPKDMRAICVHLANKVKEKHPARLASDGLRALAMEQYVHCAPGLDIYAGES 567  
 DB 405 VLKYLDPDKLRALAIINVHLETKRYVIFADCEAGLLVLEVLKLOPVYSPGDYICRKGDI 464

QY 588 VDSLFCVSGSLEVIODDEVV--AIIKSGDVFGDVFWKEATIAQS-----CANYRALTYCD 641  
 DB 465 GREMYIIEKGKLAIVADGVTQVFLSDGSYFGEISILNIKSGAKNRRRANIRSIGSD 524  
 QY 642 LHVYKDALQKYLEFF---TAFSHSFRNLILTYNLRKRYVFKSIDYKREE----- 691  
 DB 525 LPLCLSDDDIMEALTEYDPKAMLEEKQKQILMKDGLDILEVANIISDPKIDEEKVAYMEG 584  
 QY 692 --ERMRKNEAPILPPDPHVRRLPQRFRO-OKEARHAEKRGDDDD 738  
 DB 585 SMRLQTK-FARLLAEYDAQAQKLRKRLTQIEKILKVPWEQEPLEDEAD 633  
 RESULT 13  
 CNG1\_HUMAN STANDARD; PRT; 686 AA.  
 AC P29973; Q16485; Q16279;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CNGM-GATED CATION CHANNEL PROTEIN (CYCLIC NUCLEOTIDE GATED CHANNEL,  
 DE PHOTORECEPTOR) (CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 1) (CNG CHANNEL  
 DE 1) (CNG-1) (CNG1).  
 GN CNGA1 OR CNCG1 OR CNCG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Retina;  
 RX MEDLINE=92210603; PubMed=1372902;  
 RA Pittler S.J., Lee A.K., Altherr M.R., Howard T.A., Seldin M.F.,  
 RA Hurwitz R.L., Wasmuth J.J., Baehr W.;  
 RT Primary structure and chromosomal localization of human and mouse  
 RT rod photoreceptor cGMP-gated cation channel.";  
 RL J. Biol. Chem. 267:6257-6262(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Retina;  
 RX MEDLINE=92356211; PubMed=1379636;  
 RA Dhallan R.S., Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,  
 RA Yau K.-W., Nathans J.;  
 RT "Human rod photoreceptor cGMP-gated channel: amino acid sequence,  
 RT gene structure, and functional expression.";  
 RL J. Neurosci. 12:3248-3256(1992).  
 RN [3]  
 RP SEQUENCE OF 313-573 FROM N.A.  
 RX MEDLINE=95175019; PubMed=7532814;  
 RA Distler M., Biel M., Flockeiz V., Hofmann F.;  
 RT "Expression of cyclic nucleotide-gated cation channels in non-sensory  
 RT tissues and cells.";  
 RL Neuropharmacology 33:1275-1282(1994).  
 RN [4]  
 RP VARIANT ARR PHE-316, AND VARIANTS GLN-28 AND ASN-114.  
 RX MEDLINE=96036047; PubMed=7479749;  
 RA Dryja T.P., Finn J.T., Peng Y.-W., McGee T.L., Berson E.L., Yau K.-W.;  
 RT "Mutations in the gene encoding the alpha subunit of the rod  
 RT cGMP-gated channel in autosomal recessive retinitis pigmentosa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181(1995).  
 CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN  
 CC COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS A-PROTEIN CAN  
 CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION  
 CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD  
 CC PHOTORECEPTORS.  
 CC -1- SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER. FORMS HETEROOLIGOMERIC  
 CC COMPLEX WITH CNG4.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.  
 CC -1- DISEASE: DEFECTS IN CNGA1 ARE A CAUSE OF AUTOSOMAL RECESSIVE  
 CC RETINITIS PIGMENTOSA (ARRP). A DISEASE THAT LEADS TO DEGENERATION  
 CC OF RETINAL PHOTORECEPTOR CELLS.

CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC -1- DATABASE: NAME-Mutations of the CNGB1 gene.  
 CC NOTE-Refine International's Scientific Newsletter:  
 CC WWW="http://www.irpa.org/sci-news/cnbaumut.htm".  
 CC -----  
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 CC -----  
 CC EMBL: M84741; AAA52010.1; ALT\_INT.  
 CC EMBL: S42457; AAB23778.1; -  
 CC EMBL: S76062; AAD14206.1; -  
 CC PIR: A42161; A42161.  
 CC MIM: 123825; -  
 CC InterPro: IPR000595; -  
 CC InterPro: IPR002025; -  
 CC Pfam: PF00914; CNG\_membrane; 1.  
 CC Pfam: PF00027; CNGP\_binding; 1.  
 CC PROSITE: PS00888; CNGP\_BINDING\_1; 1.  
 CC PROSITE: PS00889; CNGP\_BINDING\_2; 1.  
 CC PROSITE: PS50042; CNGP\_BINDING\_3; 1.  
 CC Ionic channel: Ion transport; CAMP-binding; Transmembrane;  
 CC Multigene family; Vision; Disease mutation; Polymorphism;  
 CC Retinitis pigmentosa.  
 CC -----  
 CC DOMAIN 1 160  
 CC FT TRANSMEM 161 181 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 182 194 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 195 213 H2 (POTENTIAL).  
 CC FT DOMAIN 214 237 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 238 257 H3 (POTENTIAL).  
 CC FT DOMAIN 258 295 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 318 318 H4 (POTENTIAL).  
 CC FT DOMAIN 319 370 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 371 390 H5 (POTENTIAL).  
 CC FT DOMAIN 391 474 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 475 495 H6 (POTENTIAL).  
 CC FT DOMAIN 496 686 CYTOPLASMIC (POTENTIAL).  
 CC FT NP\_BIND 483 605 CGMP (POTENTIAL).  
 CC FT BINDING 542 542 CGMP (POTENTIAL).  
 CC FT BINDING 557 557 CGMP (POTENTIAL).  
 CC FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT VARIANT 28 28 R -> Q.  
 CC FT VARIANT 114 114 /FTid=VAR\_009295.  
 CC FT VARIANT 114 114 D -> N.  
 CC FT VARIANT 316 316 /FTid=VAR\_009296.  
 CC FT VARIANT 316 316 S -> F (IN ARRP).  
 CC FT CONFLICT 46 46 /FTid=VAR\_009297.  
 CC FT CONFLICT 85 85 S -> Y (IN REF. 1).  
 CC FT CONFLICT 146 147 L -> I (IN REF. 1).  
 CC FT CONFLICT 539 539 EE -> HH (IN REF. 1).  
 CC FT CONFLICT 677 678 Y -> T (IN REF. 1).  
 CC FT CONFLICT 677 678 GA -> WS (IN REF. 1).  
 CC SEQIDENCE 686 AA; 79126 MW; E5200D216FC97AF6 CRC64;  
 CC -----  
 CC Query Match 8.1%; Score 404.5; DB 1; Length 686;  
 CC Best Local Similarity 23.6%; Pred. No. 1.1e-18;  
 CC Matches 126; Conservative 106; Mismatches 229; Indels 73; Gaps 14;

CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC -1- DATABASE: NAME-Mutations of the CNGB1 gene.  
 CC NOTE-Refine International's Scientific Newsletter:  
 CC WWW="http://www.irpa.org/sci-news/cnbaumut.htm".  
 CC -----  
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 CC -----  
 CC EMBL: M84741; AAA52010.1; ALT\_INT.  
 CC EMBL: S42457; AAB23778.1; -  
 CC EMBL: S76062; AAD14206.1; -  
 CC PIR: A42161; A42161.  
 CC MIM: 123825; -  
 CC InterPro: IPR000595; -  
 CC InterPro: IPR002025; -  
 CC Pfam: PF00914; CNG\_membrane; 1.  
 CC Pfam: PF00027; CNGP\_binding; 1.  
 CC PROSITE: PS00888; CNGP\_BINDING\_1; 1.  
 CC PROSITE: PS00889; CNGP\_BINDING\_2; 1.  
 CC PROSITE: PS50042; CNGP\_BINDING\_3; 1.  
 CC Ionic channel: Ion transport; CAMP-binding; Transmembrane;  
 CC Multigene family; Vision; Disease mutation; Polymorphism;  
 CC Retinitis pigmentosa.  
 CC -----  
 CC DOMAIN 1 160  
 CC FT TRANSMEM 161 181 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 182 194 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 195 213 H2 (POTENTIAL).  
 CC FT DOMAIN 214 237 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 238 257 H3 (POTENTIAL).  
 CC FT DOMAIN 258 295 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 318 318 H4 (POTENTIAL).  
 CC FT DOMAIN 319 370 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 371 390 H5 (POTENTIAL).  
 CC FT DOMAIN 391 474 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 475 495 H6 (POTENTIAL).  
 CC FT DOMAIN 496 686 CYTOPLASMIC (POTENTIAL).  
 CC FT NP\_BIND 483 605 CGMP (POTENTIAL).  
 CC FT BINDING 542 542 CGMP (POTENTIAL).  
 CC FT BINDING 557 557 CGMP (POTENTIAL).  
 CC FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT VARIANT 28 28 R -> Q.  
 CC FT VARIANT 114 114 /FTid=VAR\_009295.  
 CC FT VARIANT 114 114 D -> N.  
 CC FT VARIANT 316 316 /FTid=VAR\_009296.  
 CC FT VARIANT 316 316 S -> F (IN ARRP).  
 CC FT CONFLICT 46 46 /FTid=VAR\_009297.  
 CC FT CONFLICT 85 85 S -> Y (IN REF. 1).  
 CC FT CONFLICT 146 147 L -> I (IN REF. 1).  
 CC FT CONFLICT 539 539 EE -> HH (IN REF. 1).  
 CC FT CONFLICT 677 678 Y -> T (IN REF. 1).  
 CC FT CONFLICT 677 678 GA -> WS (IN REF. 1).  
 CC SEQIDENCE 686 AA; 79126 MW; E5200D216FC97AF6 CRC64;  
 CC -----  
 CC Query Match 8.1%; Score 404.5; DB 1; Length 686;  
 CC Best Local Similarity 23.6%; Pred. No. 1.1e-18;  
 CC Matches 126; Conservative 106; Mismatches 229; Indels 73; Gaps 14;





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OM protein - protein search, using sw model

Run on: August 4, 2001, 11:35:21 ; Search time 16.92 Seconds  
(without alignments)  
1170.680 Million cell updates/sec

Title: US-09-694-777-3

Perfect score: 5001  
Sequence: 1 MTMAGRRGLVAPONTFLEN.....LFEISRPQSESEIDIFGAS 962

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCFUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1415	28.3	1159	2	US-08-956-242-13 Sequence 13, Appl
2	1415	28.3	1159	3	US-09-351-215-13 Sequence 13, Appl
3	1415	28.3	1159	4	US-09-226-012-2 Sequence 2, Appl
4	1415	28.3	1159	4	US-09-226-012-4 Sequence 4, Appl
5	1216.5	24.3	888	2	US-08-956-242-4 Sequence 4, Appl
6	1216.5	24.3	888	3	US-09-351-215-4 Sequence 4, Appl
7	873.5	17.5	626	2	US-08-956-242-2 Sequence 2, Appl
8	873.5	17.5	626	3	US-09-351-215-2 Sequence 2, Appl
9	122	2.4	539	1	US-08-464-340A-13 Sequence 13, Appl
10	119	2.4	1984	3	US-08-836-325-10 Sequence 10, Appl
11	116.5	2.3	336	3	US-08-749-816-2 Sequence 2, Appl
12	115.5	2.3	1969	3	US-08-836-325-16 Sequence 16, Appl
13	114	2.3	411	4	US-09-226-080-6 Sequence 6, Appl
14	113	2.3	861	1	US-08-484-105-18 Sequence 18, Appl
15	113	2.3	861	1	US-08-484-105-18 Sequence 18, Appl
16	111	2.2	411	4	US-09-236-080-2 Sequence 2, Appl
17	110.5	2.2	955	2	US-08-428-414A-3 Sequence 3, Appl
18	107	2.1	1989	3	US-08-836-325-12 Sequence 12, Appl
19	107	2.1	2233	2	US-08-569-853-2 Sequence 2, Appl
20	106.5	2.1	1147	1	US-08-144-121-3 Sequence 3, Appl
21	106.5	2.1	1147	2	US-08-735-893-3 Sequence 3, Appl
22	106.5	2.1	1165	2	US-08-144-121-2 Sequence 2, Appl
23	106.5	2.1	1165	2	US-08-735-893-2 Sequence 2, Appl
24	106.5	2.1	1171	1	US-07-828-788A-6 Sequence 6, Appl
25	106.5	2.1	1171	1	US-08-278-685-2 Sequence 2, Appl
26	106.5	2.1	1171	1	US-08-277-721-2 Sequence 2, Appl
27	106.5	2.1	1171	1	US-08-277-721-4 Sequence 4, Appl

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30	106.5	2.1	1171	5	PCR-US92-11337-6 Sequence 6, Appl
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37	106.5	2.1	2161	2	US-08-311-363-2 Sequence 2, Appl
38	105	2.1	2233	2	US-08-569-853-1 Sequence 1, Appl
39	105	2.1	2233	3	US-08-987-439-1 Sequence 1, Appl
40	104.5	2.1	955	1	US-08-006-676B-1 Sequence 1, Appl
41	104.5	2.1	955	1	US-08-282-845-2 Sequence 2, Appl
42	104.5	2.1	955	5	PCR-US94-00324-1 Sequence 1, Appl
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44	104.5	2.1	2101	1	US-08-470-950-4 Sequence 4, Appl
45	104.5	2.1	2101	1	US-08-467-781-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-956-242-13  
: Sequence 13, Application US/08956242C  
: Patent No. 5986081  
: GENERAL INFORMATION:  
: APPLICANT: Ganetzkly, Barry S.  
: TITLE OF INVENTION: Polynucleotides Encoding Herg-3  
: FILE REFERENCE: 960296, 94550  
: CURRENT APPLICATION NUMBER: US/08/956, 242C  
: CURRENT FILING DATE: 1997-10-22  
: NUMBER OF SEQ ID NOS: 13  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 13  
: LENGTH: 1159  
: TYPE: PRT  
: ORGANISM: Homo sapien  
US-08-956-242-13

Query Match	28.3%	Score 1415	DB 2	Length 1159
Best Local Similarity	30.1%	Pred. No. 1.6e+124		
Matches 357	Conservative 164	Mismatches 316	Indels 350	Gaps 28
QY	7	RRGLVAPONTFLENIVRR--SNDTFVVLGNAQIWPPIYVNDGFCCKLSGYHRAEVMOKS 64		
DB	4	RRGHVAPONTFLEDTILIRKFEQGRKFIITANAVENCAYICNDGFCCLGYSRAEVMQRP 63		
QY	65	STCSFMVGLDIDKDTIEVROTENYENNSFEILMYKKNRTPWFVKIAPIRNODKVV 124		
DB	64	CTCDLHHPGPRQRAAAQIAQLLGAERKVEIARYRKDGSCFLCLVDVVPVKNBDGAVI 123		
QY	125	LELCFCS----- 131		
DB	124	MTILNFVYMEKDWGSPAHDTNHRGPPTSWLAPGRKTFRLKLALLATARESSVRS 183		
QY	132	-----DITAFKQPIE-----DDSCGKMGKPARLTRL----- 158		
DB	184	GAGGAGAGAYVVDVLTLPAPSSSLALDEVTAMDNDHVAIGLP-AEERFALVGGSPPR 242		
QY	159	-----TSSR-----GVL----- 165		
DB	243	SAPQLPSPRAHSLNPDASGSSCLARTRRSCASVRRASSADDIEAMRGVLPPPRH 302		
QY	166	-----OQLAPS 171		
DB	303	ASTGAMHPLRGLNSTSDSLVRYRTISKIPQITLNFVDLKGDFLASPTSDBRIIAPK 362		
QY	172	VOKGNVNR-HSRLAEVQLQSDILPQYKQAEKPRPHIILHYCVFKTTWMIILIFY 230		



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Db 363 IK--ERTHNTKVTQVUSLGDADVPEYKLAQRIHRTILHSPFKAVMDLILLVIV 420
OY 231 TAILVYVNSEKTRQNNVA-----WLVDYSYDVIFLVYDVLNFTTEVPAG 278
Db 421 TAVFTPYSAFLKTEGEPATECGYACQPLAVVDLYIDIMFIDILNFTTYVNAME 480
OY 279 EYISDPKLRNMYLKTWVIDLSCLPYDVYNAFENDEGISLFSKLVRLGRVA 338
Db 481 EVVSHPGRIAVHYFKGMFLDMVVAIPEDDL----IFGSGSEELIGLKTARLLRYVA 536
OY 339 RRLDHYIEGAVALVLLVCVEGLAAHMAACIWSIGDYEIPEDKRTINNMLVOLAND 398
Db 537 RRLDHYIEGAVALVLLVCVEGLAAHMAACIWSIGDYEIPEDKRTINNMLVOLAND 398
OY 399 IGTPYOFNGSGKMEGPKNSVYISLFTMTSLTSVGFNIAVSTDIKIFAVAIM 458
Db 593 IGKPY--NSSGL-----GGPSIKDKYVTFALYFTFSSLTSVGFNIAVSTDIKIFAVAIM 458
OY 459 IGSLLYATIFGNVTTIFQOMYANTNRHHEMLNSVDFELKLYOVPGKLSRVMDYIVSTWS 518
Db 647 IGSLLYATIFGNVTTIFQOMYANTNRHHEMLNSVDFELKLYOVPGKLSRVMDYIVSTWS 518
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Db 867 ---MIPSGPSTLEGGESRQRRKLSFR--RTDKDTEQ----- 901
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OY 819 KSEDNNKYSKASMETLPERTKA-----SEBANTL-----KRTDSCD--- 854
Db 929 BESPSSGPSSPESSEDEGPGSRSSPLRLVFPSSPRPGEPGELMEDECKSSDTCNPIS 988
OY 855 ---SGITKSDLDLVY---GEARSPQ--DRSPILAEVKHSFPIPIQOTQATVLEVRHRL 906
Db 989 GAFSGVS-----NIFSWGDSRGROYOELPRCPAPTPSLNIP--LSSPGRPRPGDV 1038
OY 907 KEDIKALNAKMTNIEKOLS---ELIRILTSRRSSQSPOLFEISR 949
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; ORGANISM: Homo sapien
US-09-351-215-13

Query Match
Best Local Similarity 30.1%; Pred. No. 1,66-124;
Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps 28;

OY 7 RRLVAPQNTFLENIYVR--SNDTNEVLGNAQIVDPPIYVNSGFCGLGHRAYEMOKS 64
Db 4 RRGHVAPOMTFEDTILIRKEGOSRKFIANARENCNAVICYNDGFCGLGYSABEMORP 63
OY 65 STCSFMYGELTQDKTIEKYRQFTENEMNSFETLMKKNTPVWFVKAPLIRNEDOKV 124
Db 64 CTCDPFLHGPRTORRAAQAIALGAEERKVEIAFYFRKDGSCFLVDVYPVKNEDGAVI 123
OY 125 LPLCTPS----- 131
Db 124 MFLNFEVYMEKDMVSGSPADHTNHRGPPYSWLAPRAKTFRLKPLALTARESSVRSG 183
OY 132 -----DITAFKQPIE-----DSCGKMGKFAFLTRAL----- 158
Db 184 GAGGAGAPGAVVVDVLTTPAAPSSESLADEVTAMDNHVALGCP--AEERALVPGSPPR 242
OY 159 -----TSR----- 165
Db 243 SAPGQLSPRAHSLNDPASGSSCLARTSRSCASVRRASSADIEAMRAGVLPPEPRH 302
OY 166 ----- 171
Db 303 ASTGAMHPLRSLNSTSDSLVRYRTISKIPQITLNFVDLKDDPLASPTSPREITAPK 362
OY 172 VQGENVHK--HSRLAEVLOQSDILPOYKQAEKTPPHILHCVFTWMDWIIILTFY 230
Db 363 IK--ERTHNTKVTQVUSLGDADVPEYKLAQRIHRTILHSPFKAVMDLILLVIV 420
OY 231 TAILVYVNSEKTRQNNVA-----WLVDYSYDVIFLVYDVLNFTTEVPAG 278
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OY 279 EYISDPKLRNMYLKTWVIDLSCLPYDVYNAFENDEGISLFSKLVRLGRVA 338
Db 481 EVVSHPGRIAVHYFKGMFLDMVVAIPEDDL----IFGSGSEELIGLKTARLLRYVA 536
OY 339 RRLDHYIEGAVALVLLVCVEGLAAHMAACIWSIGDYEIPEDKRTINNMLVOLAND 398
Db 537 RRLDHYIEGAVALVLLVCVEGLAAHMAACIWSIGDYEIPEDKRTINNMLVOLAND 398
OY 399 IGTPYOFNGSGKMEGPKNSVYISLFTMTSLTSVGFNIAVSTDIKIFAVAIM 458
Db 593 IGKPY--NSSGL-----GGPSIKDKYVTFALYFTFSSLTSVGFNIAVSTDIKIFAVAIM 458
OY 459 IGSLLYATIFGNVTTIFQOMYANTNRHHEMLNSVDFELKLYOVPGKLSRVMDYIVSTWS 518
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OY 855 ---SGITKSDLRDLNV-----GEARSPQ-DRSPILAENVKHSFYPIPEOTLOATVEVRHEL 906
Db 989 GAFSGVS-----NIFSFGDSRGROYELPRCPAPPTSLNIP-----LSSPGRPRGDV 1038
OY 907 KEDIKALNAKMTNIEKOLS-----EILRLTSRRSSQSPQELFEISR 949
Db 1039 ESRDALQRLNRLLETRLSADMATVQLL-QRQMTLVPPAYSAVTTP 1084

RESULT 3
US-09-226-012-2
; Sequence 2, Application US/09226012
; Patent No. 6207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; EARLIER FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-226-012-2

Query Match 28.38; Score 1415; DB 4; Length 1159;
Best Local Similarity 30.18; Pred. No. 1.6e-124;
Matches 357; Conservative 164; Mismatches 316; Indels 350; Gaps 28;

OY 7 RRGVAPONTFLENIVR--SNDTNFVLGNAOIVDMPIVSGNDGFCXSGYHRAEVMQKS 64
Db 4 RRGVAPONTFLEDTITIRFEGOSKRFTIANAKVENCAYITCNDGCELCGSRAEVMQRP 63
OY 65 STGSFMYGELTDKDTIEKVRQTFENYEMNSFEILMYKKNRTPVWFVKIADIRNEDQVV 124
Db 64 CTODFLGPRQRORAAQIQAALLGAERKEIAFYRKDSCFLCIVDVYVKNEDGAVI 123
OY 125 LFLCTFS----- 131
Db 124 MFLINFEVMEKDVGSPAHDTNHRGPTSWLAPGAKTFRLKLPALLATARESSVRS 183
OY 132 -----DITAFKQPIE-----DOSCKMGKFAKRLTRAL----- 158
Db 184 GAGGAGAGVAVVDVLTLPAPSSSESLALDEVTAADNHVAGLGP-AEERRALVGGSPPR 242
OY 159 -----TSSR-----GVL----- 165
Db 243 SARQQLPSPRAHSLNPPASGSSCSLARTRSRSCASVARRASADDIEMARAGVLRPPRRH 302
OY 166 ----- 171
Db 303 ASTGAMHPLRSGLLNSTSDSLVRYRTISKIPQTLNFDVKLGDPELASPTSDREIIPK 362
OY 172 VQGENVHK-HSRLAELVQLQSDLLPQKQAPRTPHIILHYCVKTKTMMIILTFY 230
Db 363 IK--ERTHNTEKTVQLVLSGLADVLPEKIQAPRIHRTIILHYSPEFKAVMDLILLLVY 420
OY 231 TAILVPNVSFKTRQNNVA-----MLVVDSTVVDVIFLVDTIYNHHTFVVGAG 278

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Db 421 TAVFTPYSAFLFKETECPATECGYACQPIAVDVLIVIMEIVDILINFRTYVANE 480
OY 279 EYISDPKLRMYNYLKTWFIIDLSCLPYDVYANFENVNDEGISLSFKVVRLLRGRVA 338
Db 481 EYVSHPRGRLAIVHYFKGFWLIDVYALIPEDL-----IFGSGSELLIGLTKRLRLVRA 536
OY 339 RRLDIYEYGAANVLVLCVFGIAAHMMACIWTYSIGDYEIFEDFTTIRNNSWLYOLAM 398
Db 537 RKLDRSEYGAANVLFLMCTPALIAHMLACIWAIONMEQPHNDSRI-----GWLHNLGDQ 592
OY 399 ICTPIQFNGSGGKWEKGSKNSVYISLFTWTSLSLVGFGNIADSTDIKIFAVAIIM 458
Db 593 ICKPY--NSSGL-----GGPSIKDKYVTALYTFESSLTSVGFQVNSPNTSEKIFISICVML 646
OY 459 TCSLYATIEGVNTTFEQMANTNRYHEMLNSVROFLKIQYPKLSEVMYDIYSTWS 518
Db 647 TCSLMTASTIEGVNSALTIQRLYSGTAYHYQMLVREPIRHOQIPNRLRQLETFQHWMS 706
OY 519 MSRGIDTEKVLQICPKDMRADICVHLNRKVFKEHPARLASDCLRALAMEFQTVHCAFG 578
Db 707 YNNGIDMANVLKGFPECLADICHLNRSGLQCKRFKRGATKGLRALAMKFTTHAPRG 766
OY 579 DLIYAGESVDSLCEYVSGSLEVYQDEEVAILGKQDVFGDVFEMKATTAQSCANYRAL 638
Db 767 DTLVHAGDLTLALYFISRSIEILRGDVYVAILGKNDICEPPLNLYARPGKSNQDVRL 826
OY 639 YODLVIKRDALQKYLEFTAFSHSRNLILTYNLRKRIKIVPKIDVYREEERKRN 698
Db 827 YODLRIKRDLDLEVIDMPEFSDHFWSLLETENLR-----DTN----- 866
OY 699 EAPLILPDPHVRLLFORROOKEARLAERCGRDLDLVEKGNVLTETHASANSLVKA 758
Db 867 -----MIFGSPGSTELEGGRSQRKRLSPRR-----RTDQDTEQ----- 901
OY 759 SVYTVRESPATPVSPQASTSGVPDHAKLQAPGSECLGPKGGGCAKRRSMAREFDACG 818
Db 902 -----PGEVSALGPRAGAGPSSSRG-----RPGGPMG 928
OY 819 KSEDNKKVSKAEMETLPERTKA-----SGEATL-----KRTDSCD--- 854
Db 929 ESPSSGSSPSSSEDEGPGSSPLRLVPSSPPRPGEPGPELMEDEKSSDTCNPUS 988
OY 855 ---SGITKSDLRDLNV-----GEARSPQ-DRSPILAENVKHSFYPIPEOTLOATVEVRHEL 906
Db 989 GAFSGVS-----NIFSFGDSRGROYELPRCPAPPTSLNIP-----LSSPGRPRGDV 1038
OY 907 KEDIKALNAKMTNIEKOLS-----EILRLTSRRSSQSPQELFEISR 949
Db 1039 ESRDALQRLNRLLETRLSADMATVQLL-QRQMTLVPPAYSAVTTP 1084

RESULT 4
US-09-226-012-4
; Sequence 4, Application US/09226012
; Patent No. 6207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; EARLIER FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-226-012-4

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Query Match	28.3%;	Score 1415;	DB 4;	Length 1159;
Best Local Similarity	30.1%;	Pred. No. 1.6e-124;		
Matches 357;	Conservative 164;	Mismatches 316;	Indels 350;	Gaps 28

[illegible]

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0Y      819 KSEDMNNAVSKAESMETLPERTKA-----SGCATV-----KTDSCD--- 854
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Db      929 ESPSSGSSPSSSDDEBPGRSSSPLRVFPSSRPGRPEPPGEPLMEDECKSSDTICNPLS 988
          :|::||::||::||::||::||::||::||::||::||::||::||:
0Y      855 --SGTRKSRLDLDNV----GEARSPQ-DRSPILAEVKHSFYPIPBOTLOATVLEVRHEL 906
          ||::||::||::||::||::||::||::||::||::||::||::||:
Db      989 GAFGAGVS-----NIPSFNGDSRGROYELPRCPAPPTPSLLNI P-----LSSGRRPRGDV 1036
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0Y      907 KEDIKALMAKMTNIKOLS----EILRIILTSRRSSSQSPOLEFIISNP 949
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Db      1039 ESRDALOROLINRLERLSADMATVIOLL-QROMTLVPPAYSAVTTP 1084

RESULT      5
US-08-956-242-4
; Sequence 4, Application US/08956242C
; Patent No. 5986081
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/08/956,242C
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (133)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
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; NAME/KEY: unsure
; LOCATION: (593)

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US-08-956-242-4

Query Match	24.38;	Score 1216.5;	DB 2;	Length 888;
Best Local Similarity	35.58;	Pred. No. 6.1e-106;		
Matches 296;	Conservative 151;	Mismatches 292;	Indels 95;	Gaps 26

[illegible]

CURRENT APPLICATION NUMBER: US/09/351,215  
CURRENT FILING DATE: 1999-07-12  
EARLIER APPLICATION NUMBER: 08/956,242  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 888  
TYPE: PRT  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (133)  
OTHER INFORMATION: Unidentified at time of filing  
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NAME/KEY: unsure  
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NAME/KEY: unsure  
LOCATION: (662)  
OTHER INFORMATION: Unidentified at time of filing  
US-09-351,215-4

Query Match 24.3%; Score 1216.5; DB 3; Length 888;  
Best Local Similarity 35.5%; Pred. No. 6,1e-106;  
Matches 296; Conservative 151; Mismatches 292; Indels 95; Gaps 26;

OY 168 LABSVQ-KGENVHRKSHSLAELVQLGSDILPOYKQDAPKTPPHILHVCVETKTDWIIILI 226  
DB 2 IAPKVKDRTHNVE--KVTVLSLGADVLPDEYKIQTPRINKFTILHVSFRAVVDMLILL 59  
OY 227 LTFYTAIVPYNSF-----KTRQNNVAML---VYDSIVDYIFLVDIYLVNHTTFVG 275  
DB 60 LVITYTALFTPYSAFLNDRBEOKRREGYSCSPLVNVVDLVDIMFTIDILINRTTYVN 119  
OY 276 PAGEVISPDLIRKMYKTFVVDLSCLPYDVINAFENDEGSSISFSSLUKVVRLRLG 335  
DB 120 QNEEVVSDPAKIAKHVYKGFLLDMVAIIPDDL-IFSGSGDETTTLGLKTKARLRLV 178  
OY 336 RVARKLDHYIEGAVALVLLVCVGLAAHMMACIMYSIGVE--IFDEDTKTIRNSWL 392



QY 295 WFLIDLSCLPYDVINAEENDEGISSLEFSSLKVVRLRLGKVAARKLDHYIEYGAVALVL 354  
 Db 218 WFLIDMVAIFEDLL-IRFTGSDSETTLLGLTKTARLLRLVAVARKLDREYSEGAVALFL 276  
 QY 355 LVCVFGLAHMAACIWSYIGDEIFEDEDTKTRNNSWLYOLAMDIGTPYQFNGSSSGKKE 414  
 Db 277 LMCFFALAHMLACIWAIGNVERPYLEHKT---GMLDSLAVQJGKR--NGSDPA-- 327  
 QY 415 GSPKNSVYISLFTYMTSLTSGFGNIAPSTDIKIFAVALIMIGSLLYATIPGNVTI 474  
 Db 328 GSPVQDKYVALITFTPSLTSVGFGNVSPNTNSEKVSICMLIGSLMYASIPGNVSI 387  
 QY 475 FOQMYANTNRYHEMLNSVDFLKLTVYQPKGLSEVRMDYITVTSWMSRGIDTEKVLQICPK 534  
 Db 388 IORLYSGTARYHOMLRVKEFRPHQIPMLQRLLEYFQHAMVITYNGID----- 437  
 QY 535 DMRADICHLN-----RKVREHFAFLASDGCLRALAMEQ 571  
 Db 438 -----MNNXXXXXXXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 488  
 QY 572 TVHCAPGLIYHAGESVDSLFCFVSGSLEVIQDDEVVAILGKGVFGDVFKMCAATLAOSC 631  
 Db 489 XX 548  
 QY 632 ANVRLATYCDLHVIRKDALOKVLEFYTAFSHSFSRNLITFYNLR 675  
 Db 549 ADVRALTYCDLHKIQIRADLEVLDMYPAFAESFWSKLEVTFLNR 592

RESULT 9  
 US-08-464-340A-13  
 ; Sequence 13, Application US/08464340A  
 ; Patent No. 5710019

GENERAL INFORMATION:  
 APPLICANT: LI, ET AL.  
 TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,340A  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/08449  
 FILING DATE: 28 JUL 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FERRARO, GREGORY D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-415  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 539 AMINO ACIDS  
 TYPE: AMINO ACID  
 STRANDEDNESS:  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PROTEIN  
 US-08-464-340A-13

Query Match 2.4%; Score 122; DB 1; Length 539;  
 Best Local Similarity 20.8%; Pred. No. 0.01;  
 Matches 59; Conservative 46; Mismatches 86; Indels 92; Gaps 11;

QY 255 STVDYIELV-DIVLNFHT---TEVPGAGEVISDPKL-----IRNATL----- 292  
 Db 190 AIISIMFIVLSTALSLNLPLOLSIDFEGQSTNDQJLAHVEAVCIAMFTMEILFLSS 249  
 QY 293 -KTV-----FVIDLSCLPYDV-----INAFENVDCISSLSLKVVALLRL 334  
 Db 250 PKKMKFEKGPLNADLIDLALPYVTITFLTSNKSVALQFQV--RRVQIFRIMKILK 308  
 QY 335 GVARAKLD-----HYIEYGAVALVLLVCVFGLAHMAACIWSYIGDEIFEDEFTKI 386  
 Db 309 ARHSTGLQSLGFTLRSYNELGILLIFLAMGIN-----IFSSLVFAEKDED----- 355  
 QY 387 RNNSWLYOLAMDIGTPYQFNGSGSGKMGKSPKNSVYISLFTYMTSLTSGFGNIAPST 446  
 Db 356 -----DTKFKSIP-----ASFMMATITMTTGVGYDIYPKT 385  
 QY 447 DIEKIFAVALIMIGSLLYATIPGNVTITFQOMYANTNRYHEML 489  
 Db 386 LKGIYGLCCIAAGLVIALPIPIVNNFSEFYKQKROEKAI 428

RESULT 10  
 US-08-836-325-10  
 ; Sequence 10, Application US/08836325  
 ; Patent No. 6110672

GENERAL INFORMATION:  
 APPLICANT: Mandel, Gail  
 APPLICANT: Halegoua, Simon  
 TITLE OF INVENTION: Peripheral Nervous System Specific  
 TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,  
 TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational  
 TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C  
 STREET: 1100 New York Ave., N. W., Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/836,325  
 FILING DATE: 2-MAY-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/14251  
 FILING DATE: 02-NOV-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/482,401  
 FILING DATE: 07-JUN-1995  
 APPLICATION NUMBER: 08/334,029  
 FILING DATE: 02-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ludwig, Steven R.  
 REGISTRATION NUMBER: 36,203  
 REFERENCE/DOCKET NUMBER: 0917.0240002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540





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APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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FILING DATE: 02-NOV-1995
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FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein.
US-08-836-325-16

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Query Match      2.3%; Score 115.5; DB 3; Length 1969;
Best Local Similarity 20.1%; Pred. No. 0.42;
Matches 137; Conservative 94; Mismatches 220; Indels 229; Gaps 38;

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OY 145 CKGCKFKARLFRALTRSSRCVQLQALPSVOKGENVHKHSFLAVALDLSGITL--POYKOA 202
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DB 679 MSRASILNTVEELESROKCP-----W-WYFAHKLFLWNCSPWIKFK-- 723
OY 245 QNNVAMLVDSIVDYFLVDIVLNFHTTFFVG-----PAGE-----VISDPKLRNNYLTW 296
DB 724 -KCIFYIWDPRVDLAITICIVLN--TLEFNAMEHHPMTPEEFKNVLAIGLVFTGIFALEM 780
OY 297 VIDLSCLPYDVI---NAFEN--VDEGISLFF-----SSLKVVRLRLGLGVARK-- 340
DB 781 VLKILAMPYEFYQVGMNIFDSLIVTLSLVELFLADVEGLSVLRSPRLRVFLAKSMPT 840
OY 341 LDHYIE-----YGAATLVLLVCVFGLAHMMACIWSIGDYEFDDFTIRNNSML 392
DB 841 LMLIKIIGNSVGALGNLFLVLAIVFIFAVVGM-----QLFGRSYK-----ECV 885

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OY 393 VOLAMDITGPYVFNPGSGCKMEGSKNSVYISSLYFTMTSLTSGFGN-IAPSTDIK 451
DB 886 CKINDCTLP-----RW-----HMDFFHSFLIVFRVLCGMIETMDMCEV 927
OY 452 FAVA-----IMMISLTYATIF-----GNVTTIQOMAN-----TNRVHEM 488
DB 928 AGOAMCLIVMMVWVIGNLVNLFLALLSSPSSDNLPAIEDPDANNIQLAVTKIKG 987
OY 489 LNSVRDFLKY-----QVPK-----GLSERVMDYI--VSTWSMRGIDTFEVLQI 531
DB 988 INVYQTLREFILKAFSKPKISREIROAEDNTKKENIISNMTLAKMKGHFLK----- 1043
OY 532 CPKMDRADICVHLNRKVEKHPAFRLASDCCRLALAMEF-----QVHCAPG--DL-- 580
DB 1044 -EKDKISGFGSSXDKHLMED-----SDG-----QSFIHNSLVTVPIAPGESDLEM 1089
OY 581 -----IYAGESVDSLCTFYVSGSL-----EYIDDEVALVLLGKGV----- 616
DB 1090 NEELSDSDSYSKNRSSSECVTDNPLPGEGBEAEPNDEPACFTDGCVRFFSCQV 1149
OY 617 -----FGDVFNKEATLAOSCANY-----RALFYCDLHVIRDALOKV 653
DB 1150 NIESGKGKIMW---NIRKCYKIVEHSEFPIVLMILSSGALAFEDITYIEKTKIKI 1206
OY 654 LEFY-TAFSHSESRNLITY 672
DB 1207 LEYADKIFTYIFILEMLKM 1226

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RESULT 13
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217e1 Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

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Query Match      2.3%; Score 114; DB 4; Length 411;
Best Local Similarity 21.9%; Pred. No. 0.037;
Matches 90; Conservative 65; Mismatches 126; Indels 130; Gaps 22;

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OY 319 ISSLESKLAVRLRLG-RYARLRLDHYIEGAVALVLCVFGIAHMMACIWSIGDYE 377
DB 47 VSTIF-LVVVLIIIGAFAVFALEPOEISQRTTIYIQOTFIAOH--ACV----- 94
OY 378 IPEDDKTIRNNSWLQI-----AMDIG--TPYQFNSSGCKMEGSKNSVYISSLYFT 430
DB 95 -----NSTEDELILQOIVAIAINAGIIPLGNSNOVSHMDLG-----SSFEFA 136
OY 431 MTSLSVSGFNIPSPDIEKIFAVAIMIGSLYATIFGNV-----TFIFOQMYANTRYH 486
DB 137 GYVITTIIGCNISPRBEGKIFICIIYALLGIPLFGFLAAGDGLGTF----- 185
OY 487 EMLNSVRDLKLYQVPRKLSERVMDYIVSTWSMRGIDTEKVLQICPKMRADICVHLNR 546
DB 186 -----SKGIA-KVEDDFIK--WNVSO----- 203
OY 547 KYRKEHPAPRLASD-----GCLRALAMEFYVHCAPGDLIYH--AGESVDSLCTFYVSGS 598
DB 204 -----TKIRIISTIFILFGCVLFEVAL-----PAVIFKHIEGMSALDAIYFVI--T 248

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